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<p>(54) Title: BIALLELIC MARKERS</p> <p>(57) Abstract</p> <p>The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

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As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

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30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

15 A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

25 Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally PCR Technology:
10 *Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

- 5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
- 10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
- 15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
- 20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

- The direct analysis of the sequence of polymorphisms of
- 25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
- 30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

- 15 The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

- 20 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25
$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

- 30 The cumulative probability of identity ($cum p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

$$cum p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijklpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijklpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.

Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three
10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in
15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included
20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or
25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For
30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

WI-9651b	105	A T	---	---	TCTACATCTATGGACAACTCCATGCCCTTTGCACATGCTGATGCCCTCTCTCGAAATTCCTTTCCCT ACCTTGCTCCTCATGTACAATTTTCTGCTCGTCTTCAATJGGGGCAGCTTGCAGCCCTCCCTTTTAGAC ACCTCAGAGGTACAGCCGACCATGCCCTACCTCCATGCGACTGCCAGGGACCCCTTATAGGCGCTCTG CTTTAAACCTGTAAATGGTATATTAATCTTTGGTGTGTTGAATGTCCTC
WI-9651	139	T C	---	---	TCTACATCTATGGACAACTCCATGCCCTTTGCACATGCTGATGCCCTCTCTCGAAATTCCTTTCCCT ACCTTGCTCCTCATGTACAATTTTCTGCTCGTCTTCAAGGGCAGCTTGCAGCCCTCCCTTTAGACACCT CTTCACAGGTACAGCCGACCATGCCCTACCTCCATGCGACTGCCAGGGACCCCTTATAGGCGCTCTG CTTTAAACCTGTAAATGGTATATTAATCTTTGGTGTGTTGAATGTCCTC
WI-7676b	309	A C	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCTTCTGCTGGGGACTTGGCCCTGCTATTTATTTT TATTTATGCTTAATCTCTCCACTGATGCATCTCCAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCTGCTCTTCTGCTGCTGCTGGTTCAGGGCAGGAAGCTGTGGACTGCAGCTTCTGCTGTGCTG TCCCGCTGCTCTCTGAGGGCAGTATAGAGAGAGAGCAAGGATGAGT
WI-7676	139	C T	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCTTCTGCTGGGGACTTGGCCCTGCTATTTATTTT TATTTATGCTTAATCTCTCCACTGATGCATCTCCAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCTGCTCTTCTGCTGCTGCTGGTTCAGGGCAGGAAGCTGTGGACTGCAGCTTCTGCTGTGCTG GTGCTCCCGCTGCTCTGAGGGCAGTATAGAGAGAGAGCAAGGAT
WI-10072	105	G A	---	---	CATTATCTGCTCTGGCTGTTCATTCACITTCCTCTCTCCAAATGAAGAGGATATTTAAGCATCAAT CATCTGGCCCTTTTGTAGTTTGAATAATTTTGTGTGATGACTCTATGCACATGATAAATTTGTATA TGCCTGTCTCTATCTATCTTTGTATAGGAGTTTGGCCATGACCCCTTATAGGAGAAAAAGGA TCACCCCTTTTTCCTCACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	T C	---	---	TTGGTGTGAACCTCAGAAATATAGGAAATTAAGACAATTTGAATJTA, CjGTACCCAGGAAACAAGAG CCCTGCACCTGACCTCCAAAGGAGTCTATATCTGGCTGTTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTTCATCATCTGTATCCAGGCTAGTACTCACAAGAAACATGTCA ATATCAATAGCATGCATAGGGGTGTGGATCTCTTAGAACTTATGCAAT
WI-7041	174	C A	---	---	GTCTATTGCAGGAGAAADGTCCCTGGCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTGTGATGCGCTCTATTCCCGCTCTGCGCTCTCjCjACACCTCTTTTGAGCAAGGAGATGC AGCTGTATTGTGTACAAGCTCAATTTGTACAGTCTGTTCATGTATAATA
WI-7224	134	T C	---	---	ATAAACCTGTATTGTATCAACCAACTCACTAAATATCAACTTATGTGCTATCAGATATCTCTCT ACCTCAGCTTGTATTTGAAGAAATCTTAACATCAAAATACTTTCATCCATAAAATGTACGCAITTT /CjATTAAGAAACAAATCACTTTTAAAGAAACACATAAGGACACATTTTCAAAATTAATAAAAAAAG GCATTTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTATTCATGCTAG

[illegible]

WI-931c	191 C A	GACCAGGACACAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAAACCTTGACACCCCTGGAGTT TCCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCTTCT GTTGCTGACTGTCTATTCTGTTGATGGATTATTAATTGTCACAAAAGCC/CACGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-931b	81 A G	GACCAGGACACAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAAACCTTGACACCCCTGGAGTT TCCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TCCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TCCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TCCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-931	31 A G	GACCAGGACACAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAAACCTTGACACCCCTGGAGTT TCCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TCCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TCCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGCAAAATGATCCT TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-10870b	91 C T	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGAGTGGCAGA GATCCACCTTAGCAAGTGGG/CACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGATACAAATAGGACATGGGTACG CTGAGCCACTCTTAACCATGAACCATCACCATTAAATACGTTGCCCC
WI-10870	103 G A	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGAGTGGCAGA GATCCACCTTAGCAAGTGGG/CACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGATACAAATAGGACATGGGTACG CTGAGCCACTCTTAACCATGAACCATCACCATTAAATACGTTGCCCC
WI-7719b	281 T C	AGTTTATCTCCAGATGACAGCAGTAGACAAATGGATAGTACGAGAGTCTTAGGTAAAGCTT GGGAAATATTGGGCATTGGTCTGGCCAGTCTACATGTCCCAATATCAAGCACAACCCCTAGC TTCTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGACCAATATGTG ATTCTGGACATTGCCCATGTATAATCTCCTCAGTGAATTCAGCTAAAGCAA
WI-7719	163 A G	AGTTTATCTCCAGATGACAGCAGTAGACAAATGGATAGTACGAGAGTCTTAGGTAAAGCTT GGGAAATATTGGGCATTGGTCTGGCCAGTCTACATGTCCCAATATCAAGCACAACCCCTAGC TTCTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGACCAATAT GTGATTTCTGGACATTGCCCATGTATAATCTCCTCAGTGAATTCAGCTAAAGCAA
WI-10396	72 C A	GCTTGGAGTATATCTAACTGGCTCCACTTCTTTCTTGAACATTGCTATCACTGGGAA GAGTCA/TGAGTACITTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTGTTCTTTTGT TGCCATTGAGGGATGTGATGTTCTTAACTATGAAGTACTGGCTGTCTCTCCATGCTGTTGAGG TTAACAGCCACCATTTGTAAACACTTGT

WI-10673	94 C G ...			<p>TCCCTTTATGACCCCAAGAGATATTTATTAACACCAATTAAGTAGCAGGCCATGGCTCATGGGAAC CACCCCGGTGGCACTATGAGGGGGGCTGAGGTTGCAAGTTGCAACTATGCAAGTGTCCGGCCACACA TCCTGCTGGGCCCCCTACCCCTGCCCAATTCATCTGCCAATAATCCTGTCTATTTGTTTCATCTG GAGAAATGAAGGGAGGTCAAGTTGTTTGTCAATGATTTGTCAGAGAACCT</p>
WI-7842	57 T C ...			<p>CACAGCATGCCCTTGAGGAGCGGGCCACAGATGCTGAATCCCTATCCCATTCCTGTCGTATGAG TCCCATTTGCCCTTGCAATTAGCATTTCTGTCGCCCAAAAAGAAATGCTATGAAGCTTTCTTCCT ACACACTGAGTCTCTGAATGAAGCTGAAGGCTTAGTACAGAGCTAGTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA</p>
WI-7721	145 A C ...			<p>CTGCTCATCAGCCCACTGGAGTCCACACTTGAATTTTGGGCACTACCAAGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCAACCCAGCTGTACCCAGCCCGGGCAGGTGCAGCCCTTCCTCC TGTCTCTGCTGCTGCTCTTTTGGAGTCCCTCTGATGCTCTACCTCTGACTTCTGTGTCCTCTG TGTCTCTCTCATCATCTCTCTACTGGGGCTGGGGCTAGCCCA</p>
WI-4767b	173 C A ...			<p>TTTCCAGTCTGTTTATCCTTTTATGCTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCT CAGGTCTGGTAACTCTAGATCTTCTATATCCTATTGAGTGTGATGGAGTTGGAGAGGGTATGTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACAC/A/AAATCACTAAGGAATTCCTACTAAGA CTCCTTAACCCAGAGATTTTAACT</p>
WI-4767	50 A G ...			<p>TTTCCAGTCTGTTTATCCTTTTATGCTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCT CCTCAGGTCTGGTAACTCTAGATCTTCTATATCCTATTGAGTGTGATGGAGTTGGAGAGGGTATG TTTCTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCTACTAAGAC TCCTTAACCCAGAGATTTTAACT</p>
WI-7718f	222 C T ...			<p>ATTGCACTGAAGTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGT ACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATACAAAGAA/C/T/CATGCAAGGAAGGAAAACTATGTATTAA</p>
WI-7718e	60 T C ...			<p>ATTGCACTGAAGTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA GGATTACAGAACTGATGCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTCA AAAAGGAACAAAAATTACAAAGAACCTATGCAAGGAAGGAAAACTATGTATTAA</p>
WI-7718d	31 G A ...			<p>ATTGCACTGAAGTTTGAATACTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA GGATTACAGAACTGATGCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTCA AAAAGGAACAAAAATTACAAAGAACCTATGCAAGGAAGGAAAACTATGTATTAA</p>

WI-7718c	91 C G	ATTGCACCTGAAGTTTGAATACCTTTGTAGTTACTAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGGTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAATGAAGAGGAGCTGTGTTGAAACAGAAATAAGTTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAT
WI-7718b	248 A G	ATTGCACCTGAAGTTTGAATACCTTTGTAGTTACTAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGGTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ACTTGCAGATGGAAGAGGTGAATGAAGAGGAGCTGTGTTGAAACAGAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAT
WI-7718a	42 A T	ATTGCACCTGAAGTTTGAATACCTTTGTAGTTACTAAGCAGTTACTCCCTACACTGATGTC AAGGATTACAGAACTGATGCCAAGGGGCGGTGAGTTCACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAATGAAGAGGAGCTGTGTTGAAACAGAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAT
WI-7227d	99 G C	AGGGAATTGTTGCTCTCGGAGGAAGCCAGGCATCTAAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTTACAGACAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAAGCAGCTAATGCAAT
WI-7227c	291 G A	AGGGAATTGTTGCTCTCGGAGGAAGCCAGGCATCTAAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTTACAGACAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC GGTAGTCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGAGCTGAGCTAAACAGTG TTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAAGCAGCTAATGCAAT
WI-7227b	93 G T	AGGGAATTGTTGCTCTCGGAGGAAGCCAGGCATCTAAACAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTTACAGACAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAAGCAGCTAATG
WI-7227a	24 A G	AGGGAATTGTTGCTCTCGGAGGAAGCCAGGCATCTAAACAGCCAGTAGGTACCTGGCTTC TTCCGTGGACCAATTCATCTTTACAGACAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCAAGAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAAGCAGCTAATG
WI-7310b	234 A/C	CCACAATGCTCTCCAGCATGCAAGGACTCCTGCTGCTCGAGGTGGGAGACAAAGCACTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGATCCTTCAGAACAACTGATGCGAAACT TGAATCTGTACTGAAATGAGAGAGAGGACATGTCTATTGAACTGAGCCCAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCATCCCAACATGATGATCTGAGATTTC

WI-1795b	130 TC	GAAGCAACAGAAAGTATCTTTATCCCATCTAGATTATGCTGGGTCTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACCTGAGGTACTTAGATCTCAGTGCCTTGCAAGAAAGAAAGTCTC GTCTACCATTTTACCAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCTAGGAGTCTAA AGTGACTGGGAGGCGAGATT
WI-1795a	47 TC	GAAGCAACAGAAAGTATCTTTATCCCATCTAGATTATGCTGGGTCTCCAGACTCCTACGATTA TTAAATGTATGCATGTGAACAACCTGAGGTACTTAGATCTCAGTGCCTTGCAAGAAAGAAAGTCT GTCTACCATTTTACCAAATTCGTAGTACAAATTAAGTATCTCTGTTATCTCCCTAGGAGTCTAA AGTGACTGGGAGGCGAGATT
WI-10616d	136 GA	CACAAATTTGCAACACATTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAAGCTTTTACTTCCACGTCTCTCCATAGTAGTCTGCTGCTCTCTATACATTTGCCA CIGATTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGCCCGCCAGTCCCTCTCGAGACTCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136 GA	CACAAATTTGCAACACATTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAAGCTTTTACTTCCACGTCTCTCCATAGTAGTCTGCTGCTCTCTATACATTTGCCA CIGATTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGCCCGCCAGTCCCTCTCGAGACTCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141 CT	CACAAATTTGCAACACATTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAAGCTTTTACTTCCACGTCTCTCCATAGTAGTCTGCTGCTCTCTATACATTTGCCA CIGATTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGCCCGCCAGTCCCTCTCGAGACTCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116 GC	CACAAATTTGCAACACATTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCACATAGAGAAGCTTTTACTTCCACGTCTCTCCATAGTAGTCTGCTGCTCTCTATACATTTGCCA CIGATTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGCCCGCCAGTCCCTCTCGAGACTCC ATGGATCATCTCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52 GA	CTCTATTCTCTGGGACTGCTTTCTTTGGGGCAAACTCCAGTATCATCTGATCTACTATATAAAA AAACCCCTGTAAGTCTGCTGCTGCTTTTCAAGTTCATATATATCCAGTATGTTTCCAGCAAAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTTTCAGTTTCCTCAAAAGGAATATGAAT TGTTAAATGCAAAATCCAGCTGTAACCTTTTGGACTGTCTTTATTTCT

WI- 10400d	189 A G			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTTAGACATCTGCTG GTTAACTGTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCAGTCCCATGTAG TTTTTGGTTCATTTACTTGCATAATTAATCAAGGCGTTAATGCAATTATG
WI- 10400c	166 A C			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTTAGACATCTGCTG GTTAACTGTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCAGTCCCATGTAG TTTTTGGTTCATTTACTTGCATAATTAATCAAGGCGTTAATGCAATTATG
WI- 10400b	165 A G			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTTAGACATCTGCTG GTTAACTGTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAATTTT TCCTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCAGTCCCATGTAG TTTTTGGTTCATTTACTTGCATAATTAATCAAGGCGTTAATGCAATTATG
WI- 10400a	46 T C			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTTAGACATCTGCTG GCTGGTTTAACTGTATAAGATGGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTTCCCTTACCTTTACTCCTCCCAACCAAAATAACGTAAGTACCTATGTCAGTCCCATGT AGTTTTTGGTTCATTTACTTGCATAATTAATCAAGGCGTTAATGCAATTATG
WI- 10809b	78 C T			AAAGGCTACAACTAAGGCCAAACCAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCACTGTATAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATCTGTTAG CAACAATGGATGTATTAGCCCAAGCAGGGTATGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI- 10809a	33 C T			AAAGGCTACAACTAAGGCCAAACCAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGAG CCCCCTCTCACCACTTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATCTGTTAG AAACAATGGATGTATTAGCCCAAGCAGGGTATGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C			CGAGCTTGGGATAAGCAAGGGACCTTGGGCTCTACGCTTCCTGCTCCCATCCAGCTTGTGTCC CAATGAATAGTACGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGA/CJGACTGTACAGGAAGGGTCGGAGTCTGTAAACCAACGATACAGTTTGGCTTTTTCACATGAT CATTTTATATGAATAAAGATCCTGCTGCAATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C			CGAGCTTGGGATAAGCAAGGGACCTTGGGCTCTACGCTTCCTGCTCCCATCCAGCTTGTGTCC CAATGAATAGTACGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGA/CJGACTGTACAGGAAGGGTCGGAGTCTGTAAACCAACGATACAGTTTGGCTTTTTCACAT GATCATTTTATATGAATAAAGATCCTGCTGCAATTTATGGTGTAGTCTGAGTCTGAG

WI-7038a	31	G A	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[GA]CTCTCAGCTTCCCTGGCCACATCCAGCTTGTTG TCCCAATGAAATAC TGAGATGCTGGGCTGCTCTCCCTCCAGGAATGCTGGGCCCCAGGCTGGCCA GACAAGAAGACTGTAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCAATTATGGTGTAGTTCTGA
WI-3429b	64	G T	ATAGGCTTCTGCTGCTGCCACAGTGAACAGCACCCAGGTCGGGTCGGGCTCCACACAG[GT] CCCTCAGCCCCCTCAGCTTTGCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATTCCCAAGTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGGACCTCCAGGGCAATTTCTAAGACCAAGCACGGAGC
WI-3429a	62	C T	ATAGGCTTCTGCTGCTGCCACAGTGAACAGCACCCAGGTCGGGTCGGGCTCCACACAG[GT] CCCTCAGCCCCCTCAGCTTTGCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATTCCCAAGTCTCTCTCTGGATTGGATCTAGCAAGACCAGAGACGGTCTCTAGAA TCCTGACTGTTAACAGGACCTCCAGGGCAATTTCTAAGACCAAGCACGGAGC
WI-6786c	151	G A	ATTTAGGACAGTGAAAAAAGGGATTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTTGGCGAAAGGATTAAGAAAGTGAAGTGACGGTGA GTGAGCCCCATCTCTGATGGATAAGGTGTCCTATTTGTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTTGCTCAGTTTCATCAIT
WI-6786b	111	A T	ATTTAGGACAGTGAAAAAAGGGATTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTTGGCGAAAGGATTAAGAAAGTGAAGTGACGGTGA CCTGTGAGCCCCATCTCTGATGGATAAGGTGTCCTATTTGTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTTGCTCAGTTTCATCAIT
WI-6786a	106	A T	ATTTAGGACAGTGAAAAAAGGGATTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTTGGCGAAAGGATTAAGAAAGTGAAGTGACGGTGA CCTGTGAGCCCCATCTCTGATGGATAAGGTGTCCTATTTGTTGGAGGGTGAATGCCACATTTC TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTTGCTCAGTTTCATCAIT
WI-6711b	226	G T	GGCTATTGTGAATGCTTGGTTATTGACTCCAAAATGAATGAATGGGGAAGAAATCCCTCACCT ACCTTCCAAATCCCTACATATCAATTTTACAAAAGCCCCCTAAACCTCAGTCCCAATCAGTCTGAAT TTCATATACCTCCATTTAATTAATCAATACATCATTCGAGAGAAAAGACACGGTGCACACTGGGTT TGGTTGGTGCCTGCACCCACAG[GT]TGGCACTAAGTGTAACTCTCTAA
WI-6711a	36	T C	GGCTATTGTGAATGCTTGGTTATTGACTCCAAAATGAATGAATGGGGAAGAAATCCCTCACCT ACCTTCCAAATCCCTACATATCAATTTTACAAAAGCCCCCTAAACCTCAGTCCCAATCAGTCTGAAT GAATTCATATACCTCCATTTAATTAATCAATACATCATTCGAGAGAAAAGACACGGTGCACACTG GGTTGGTGGTGCCTGCACCCACAGTGGCACTAAGTGTAACTCTCTAA

WI-9826b	127 GA	AATTTATATGTGAAGGTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTGGTGTGTCACGAGTTGAGCCATTGACAGAGGCTGTATG/AJGCCTT CAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAGTTTGCTGATCTAGATATTTAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125 AT	AATTTATATGTGAAGGTAGCAAACTATGGCCACAGGCCCATCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTGGTGTGTCACGAGTTGAGCCATTGACAGAGGCTGTATG/AJGCCTT AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAGTTTGCTGATCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60 TGTGGGTTTT	TTGTTTGTGT	AAACGTAAAA	TGACATTATAT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTGTTGTGTGGGTTTTTTT/GJTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A GAG	AACTGCAAAAT	CCACCTGGGGC	GAAAATGT	TTCAAGTAACCTGCAAAATAGGAACACAGAG/AJGGGAGCCCCAGGTGGGACAAATCATGGCTACCCCG TCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCCTTAT
WI-8170b	259 GA	GCACCTCTCTCTGAGCAACAGGTACACATTTTCTCTAACATTTGATCTATAACACACCAAGACCG TGTTTAAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAAGTTAG CAITTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAGTGCAATCCCTATCAATCAGAA ATAAGGTAAAGGGCCCTCAAAATGAATCTACGGAAACATACACAAGA
WI-8170a	204 TA	GCACCTCTCTCTGAGCAACAGGTACACATTTTCTCTAACATTTGATCTATAACACACCAAGACCG TGTTTAAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAAGTTAG CAITTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAGTGCAATCCCTATCAATCAGAA AT/AJAAAGGTAAAGGGCCCTCAAAATGAATCTACGGAAACATACACAAGA
WI-8172	136 C GACA	CTTTATTAAA	GAAGAGAAAT	...	CAGGATTCCTTAAGTCATCTTCCAACTACTCCAGGTCCACATGGTGAAGTCACTGTTAAACACGAA ATCTAACCATTAACAAAGCTTTAAATCTCCGTTAAGTACTCTACCAAGATGCTGTGGTAAAGTTAG CAITTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAGTGCAATCCCTATCAATCAGAA AT/AJAAAGGTAAAGGGCCCTCAAAATGAATCTACGGAAACATACACAAGA
WI-8183	56 GA TGC	TTGAAATAAAA	TAATACCTGT	AAAGGTAC	AGCAGGGTTTGAATTTGATCCCTTATTTACATGAATAAACAATTTCTGTG/AJGACGGTT TGATTTCAACACAGTTGAATCTGTAACCAACCAAGCTGTTTCTGATGACGAGCAAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83 CT	GCCTTATTTGGGATTGCAAGCGTTTACAAGTTTAAAGACAACCCCAAGCATGGGATTTTGC CGGAAT ATTAGCGTTAAAGGAG/CJTGGATTGAGTCAACACACGGG
WI-8712	44 G A/G	CACAGGGAAG	CAGGAAGCCTG	ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGTAGTGGAG/AJGAGATGTCAGGCTTCCTG TTCTTAACAGCAGAGAGCCCAAGCAACCTAGAGAGCCCTCACTAGCCTCTTAAT

WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AACATAACCA CCTGTAAATTTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTGGTCACTTTTGGTGAAGACACATATCTGGTACAAAAT ACAGGTGGTTTATGTTCACTACATGATACAAATCATTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G GTGGGCTT	GAGAACACTT GTGGGAGGAA	GGACCTATCAG TCCATGTTTGA	ATTTTGTGGCTATAGGTGAGTGGTTCTAAACTTTGAGCTTGCAGAGAACACTTTGTGGGGCTTAA GTTCAAACATGGACTGATAGGTCCACCCACAGATTTCTAACTGGGTAGGTCTGGGGTG
WI-12345	37 C A AAAGAGAA	AAATTTTGG AAGTTTTCAG	TTCAGAGGGG TTCAGG	GGAACAGACTGATCCAGTGGCAGGAAAGAGAGAAACATCTGAAACCCCTCTGCAAGTATCTCT TTCCTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTTGCAAAA
WI-13416	71 C A AAA	AAATTTTGG AAGTTTTCAG	AGTGTATATAG TTCATGAATA	GAAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAATTTTTCAGAAAAAAATAAATGACAAGAACAA CATA[CA]AAATATTGAAATTTATTCATTGAACTATAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46 G A AAAAGC	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGGTCT	TTTGAAGAAGATGCTGAATTTATCCCAAGTATAATTTTAAAGCTTGA/TTTAGACCCCAACATA TTTAAACATCTCTACACATACAGAAATTTTCAAGTTTACAAATATTCAGAAAGGCATTTTCTTAAGCAG T
WI-12086	72 C T TTGGATT	CCGGGAAAC TTGGATT	GGAGTCTGG GTCTGG	GAACGAGCTTTATGGAGCAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAACCTTG GATTTC/TCAGAGACCCGAAGACTCTCCAAAGTCTCACTGTTAGTAAGGTCAATTTGGGGCAGA ACAGGAACATGGCTTAGCT
WI-11549	102 T G TTTTATG	GGCATAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCCC	ATGCTTCACAGGTGTATTTTGTAAAGAGTTTGTCTATCTAAATTTTCAATTTATTTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTGTTGGGATTTGTACAGACTTTTCC
WI-11585	79 T C AAACAAAA	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACCTCC	TTAGAAGGAAAGAAATAAACACAGGTAAATGGGAAATCAGTTTCAGAGGTAGGAAGGAGCTGGGT TGCAAAACAAAAATCTGGAGATTCAGTGAAGCATGGCCTAGAGTCCAAAGCAGGGGTAGAGT TT
WI-11604	68 C I	TTAGTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACAAATAGGATGTTCCAGTTACCAGCATTTT G/CJAGAACTAGGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTTCTGACGCTACCATTTTTC TTTGTACTCTGCAGTT
WI-11614c	108 C A	CAAAATCAAAATTTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTGCTGTTGAGGCAT GTTCCACCTGGACTTGGCAACTTTTCACTGTGAAACTGCAACATATAAGTATTGTCAGCTAC GGACTTCGT
WI-11614a	60 A G CAGCTGCTTG	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAC ATGCC	CAAAATCAAAATTTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTGCTGTTGA/GGG CATGTTCCACCTGGACTTGGCAACTTTTCACTGTGAAACTGCAACATATAAGTATTGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	TTGATTTTACTAAGGTCTTCCACTGGAACTGAAGGTAGGATAGGTACAGGATAATATACTCAG ATATTTTAAATAAATCTGACTTAATAATAAGAAATTAAGCAATACCACATTTGTCATTTGCTAC AAGAACAATTTGCAATGA

WI-11826a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCCTCCACTGGAAACATGAAGTAG/GA/GATAAGGTGTACAGGATAATATACT CAGATAATTTTAAATAAATAATTAATTAATAAGAAATAGCCATACCCATTTGTCATTTGCTAC AAGAACAATTTGGCAATGA
WI-11827	23	T C	CCTTCTCTC ATTGTCTC	CATTGCAAC CATCTCAAG	ACCCCTTCTTCCATTGCTCTC/CCTTGAGATGGGTGCAATGGGAAATGGAAGTAAAGCAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTCGCATGTCAAGTCCATCCATG
WI-11838	61	A G T C T	GGACTTAAAA AGATCTGCTTA	AGAACTTGGCT AAATATTTTAT GTAACACT	TCAGAAATGTGGCAAGCAATACTATTGTAAAGGTGGACTTAAAGAGATCTGCTTATCCCTAG/GTA TATCCACATACTCTAGTGTACATAAAATATTAGCAAGTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCCTTTTGGTA
WI-11837	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAGAATGAT T	GTACCAATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGGAGCTGAATAAATTACAG TATACAATATTAGAGAAATATTATGTGCAATTTGCTCATCTTACTCTGACCAT/GGATAATCATCTTT TTTGCTGGGTCCAGGACC
WI-11854	37	G C C T G	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGGCCAAAAGACTATTACAGCACTG/GC/JAAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCAGAGTTTACACTCATATTTTCATATTTT ATTTTGGGTGGTGGT
WI-11856	28	G A A	ATTGATTTTAG AAGGAACTGC	CAAGGCTTGT CCTCAAGTAAA	ACCTGATTTGATTTAGAAGGAACTGCAAG/GA/CJCTTACTTGAGGACAAAGCCCTTGCCTGCAAGTTGTTT AAAATGTCTGAAACAATCAGATTCCAGCCTGGAT
WI-11880	55	T C	TTATCACAG AGGGGACAG	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTTGAITCTCCCTTTT/CJTTGCATAAA GGCTGGGAAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11896	47	T C	TTATCACAG AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACCTTTGACATCTTTATCACAGCAGGGGACAGT/CJAAGGTTGGCTTCTCTA ATGCCACCACTCTTGTTTTCAGAACTTTTCCACTTCGCC
WI-11702	69	C T	GAATAACT GAAATAACCA	AGAACACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGCACATACCTTCAATAATTAATAAATACTGAATAACTGAAATAACCCACAGC AG/CJTTCAGTATAATTGCTGAAGTTGTTCTAGAAACACTGCTAAATTTTGTTCCTGACAGA
WI-11706	60	C T	TGGCTGGAATT TTCTCTTCT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAAATTTCTCTTCTGTACAAATTTATTTGGC/CJGGCTG GAATTTGCTTTTGGTGATTTGTCCTCTGGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAAGTTGC	TCATTTCTCT AATTTTACGGG A	AATATCATCTCATATCATGAGCATGTTTATAAAATGAGAGATTATGCTTTTGGCATACTTCTATC TTCTTCAGACACAGAGAGAGAGCTTGTCTAGTTTGT/CJAGTCCCGTAAATTTAGAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103	C A	GCACCTAGCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCGAGCTTCCAGCACCAACGAGCCACACTCTAGACACGCTTAC TCCAGTCCATCTGGCACTAGCCCTCAGTCTTCA/CJACTCCTCCCTCTCCACACTCCTTC

WI-11715b	123	C T	AGCTT	AGCTGGCTGC	TOCCATCCTG TGGCT	AGATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCATTACAACTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGAAGA
WI-11715a	49	A C	AAA	AACAATCCTT AAACAACATA TCAACA	CATTACACCAC AGTTGTAATGC A	AGATGGAGCTGTGGGAGGAGACATGCACACAATGTAAACAGACAAAATGCATTACAACTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCTAGCCAC AGGATGGGAGCTGGGAAGA
WI-11727	43	G C	TCAACA	AAACAACATA TCAACA	CCTGTGGTTTG TGTTGCAG	CTGGATTCCTATACCTAACAAATCCTTAAACAACTATCAACA[G/C]CTGCAACACAAACACAGGC AAATGAAAACAGATGCCCCAGACAGACCCACCACATGGCACACAC TTTATTTATCAAACTC[G/C]CAATTCATTCCATTACAAATGTAAAGTTATCATCAGCTCCCATCCACTTT CTCCCATCTCTTATCTCTTCCACCTACACTTCTCTCCCTACAAACCCGGGTTCCAAA TTTTCCTCTTTTATTAGTCCGCTACTACTAACTAGAGGAGAACTGTGGTTTTCGCCCTG[G/G]TAG ACCACAGGGCCCAATCACCACAGCTCTTGTAGAGACATGGAGAGTCCCAAGATCACCATCA
WI-11758	61	A G	TCGCTG	ATCTGTGGTTT TCGCTG	GAATTGGGCTT TGTTGCTA	CCGGCCTCACAAAGTATTTCTAAATATAATTTGCT[G/G]TAGAGTTTACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAAATCAGTATTTGGCTCAGCAGGAAACAGACTTTT AGCACATGATATTTCTGGCTGGAGTTTCTGTAGCTCAGCAACAGCAGAGTCAGAGATTAAAGATT ATTATTTGGCTCTTTTTCCTCTTTCCTGCTGCTGATTTGTTAATTAGGGAGTCAAGGCCAAGTTATC ATGACAAACCTCTTATTTAATGGGCTCAGAGAGCAAGGGA[G/C]GACACAAAATTTACAGTCTGA GTTTTCGGCGCAGAGACCCCTCTCCACCTTTTCATGCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11282	42	C G	GCAAGGAA	GGCTCAGAGA	AAACTCAGA CTGTAAATTTT GTGTG	TAATTCACCAACTTACCACAACTCTGT[G/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACCTACAAATGGGCAAAATCATCTAACACAAAGC
WI-11790	28	A G	AAACCTCTG	CCCAACTTACC	CGTAGGGGAG GCTAAGC	TTTAATTCCTCCAAAGCTTACAAACCTCTTTCATCTAATCTGTGAGGTATTAGTATACAG[C/A]AGT GATTTCTCTCTCTCTCTTTTATTAAGTGAAGAGGTTCAACTATCCAGAGTCCCATCTA
WI-11879	61	C A	AGTATACA	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTAATTCCTCCAAAGCTTACAAACCTCTTTCATCTAATCTGTGAGGTATTAGTATACAG[C/A]AGT GATTTCTCTCTCTCTCTTTTATTAAGTGAAGAGGTTCAACTATCCAGAGTCCCATCTA
WI-12469b	91	C T	AAGTTTAAA	GTTTTTAATGT GGTATTAGAA AAGTTTAAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTAATTCCTCCAAAGCTTACAAACCTCTTTCATCTAATCTGTGAGGTATTAGTATACAG[C/A]AGT GATTTCTCTCTCTCTCTTTTATTAAGTGAAGAGGTTCAACTATCCAGAGTCCCATCTA
WI-11906	52	A G	ATCTGAA	TGTTATAACAT CAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTTATACATCAAAAGAAAGAAATCTGAAT[G/G]TGAGGAACTG CAGAAATTAACCTTTCAGTCTAATTTCTCAGAAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTGTGTTGGG TGTCAG	CTCTCTGAG ATTCTCTGAAT AG	GCAGTCTCTGAAAGACAATGGATTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTGTGTG GGTGGTCAAGJAGTATTTCAGAAATCTCAGAGGAGGACAATGATAGTGCAGCTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAATTCA	CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCGAGTTCA/T/GIGTT TTATTAGTATATAAATTTGGCTTTACAGGAAGCATATTGG CCCTAGTGAATACAACCTTTGTCTCGAGACJCA/CCAGCTAGTCTAAGAAACTTCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGGGAA
WI-11946	31 C A	TGAAGATCAG ATCTCTGGTTT	...	ACAAAATTCACAAAGTACAACACTGCTTATTTCTCTGTTGAAGATCAGATCTCTGGTTTATTAA/T/ GATCAACATTCACACAGCTGAAGGAAATTAACCTGAACCT ACCTATTTTGAACACTGCAGAAAGGCGAGACAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTAGCTTTTAAAAAT/AAATAAATACTGTAAACACATTTCTCTATTCTCTTACGA ATAC/TCTCTTTTGTATTTGCAATTTCTATGTCATACACAGAGGCACTCTCTCAATGCCCCG TTCTGCTGAAGATCACAACAACTTTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTGTACCTTT GTGTTATTTCTGTCTTCAACTAAGGAC/TAGACTTCAGAAAGGCATAGCTTCCCTTGTAAAGCTTTT AAACATCTTTTCAITTTGTAGGAAGGAACTTCAAAAGCCCCAA
WI-11049	95 C T	AAAAGGACAG CCAGATATCA	TTTCCATCTTA TTTCAITTTCTG	CAACATTTATCAACATGGTAGGGAAGTTCTCACTCTGCACATATAAAAGGACAGCAGATATCA AC/TGTACAGAAATGAATAAGATGGAATTTTAAACAAATG
WI-15488	69 C T AC	AACAGTTAAT GAAACACATC	GGCTGGTGAAA TGATGTAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCGTA/JGIGTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAGGTAACTTTTCCCATTTTACAGACAACCCAGT ATGAGACCTGCTTTGAACGTTAAACGTTTGGTAATAATGGAAGGAGCTAGGACAATCTTGCTT TCAAGTAAATTTGTGACTGAGCAGCAAAATCAGCCAGCTATCTGGTGCAGAGAGGTACTCCAAGTA C/TGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAGGAA
WI-13654	49 A G	OGT	...	ATGAGACCTGCTTTGAACGTTAAACGTTTGGTAATAATGGAAGGAGCTAGGACAATCTTGCTT TCAAGTAAATTTGTGACTGACGACGAAATCAGCCAGCTATCTTGTGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAGGAA
WI-11070b	135 C T	CAGAAAATCA GCCAGCTATCT	TTGGAGTACCT CTCTGCAAC	AACTTTTATTTCCAGCTTTGAGACAGTATTTTGAGGCTGATTTACCTCTAGCGGCGAAACCC AGAGCCAGCTAATAAGCAGCCAGAAAGCTACAGTAATTAATGATGACCATTTTCTCTCTTTAGC ACGTCTTTGTCTCTCTC
WI-12020	121 T C	

WI-11076b	142	GA	---	---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTCTTCTTGGGAGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAGAGAG(G/A)AGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT
WI-11076a	106	TC	AGGCA	AGGGGAGC	TCCTGCTCTGG GTATGTGAC GGTTATTCAAA AATTAGTATGG GACA
WI-14263	49	TC	GGCATA	CGCAGAAAA	GGTATTCAAA AATTAGTATGG GACA
WI-14267	28	TC	---	CTTTTCATTT	GGTATTCAAA AATTAGTATGG GACA
WI-13892	50	GA	TAGAAC	TGCTTTTAAA	GGTATTCAAA AATTAGTATGG GACA
WI-15288	108	CG	TTCCCTCTCTC	CATGAGGA	GGTATTCAAA AATTAGTATGG GACA
WI-13951b	88	GC	---	GGAGTGAACA	GGTATTCAAA AATTAGTATGG GACA
WI-13951a	39	CT	CAAAA	AAGTAATGAA	GGTATTCAAA AATTAGTATGG GACA
WI-13264	25	GA	TTGCCAT	AAAAAGGCTC	GGTATTCAAA AATTAGTATGG GACA
WI-13960	39	AC	TGATAGA	AGTTAAATAC	GGTATTCAAA AATTAGTATGG GACA
WI-15843	62	CT	CAG	AAGAGCCCTT	GGTATTCAAA AATTAGTATGG GACA

WI-13983	52 G A	TCTCTCCACT CCTTAAACCT	CAATACTCTCT TAGCCACGTGG	TTGTGTCTCTGATTCGGAACATAGAAAATCTCTCTCCACTCCTTAAACCTTGAACTGGCTAA GAGAGTATTGTACAGAAATATGCACCTGACTTAACAGAAATTAAGAACATCCAGGCACTGAGAG
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTGTAA	CATGAATCTCAGGTCACAGCTTTATTTATAGATTTTAAACAGCCCATTA/GTTTACAAACATTGT CAGGGAACATTTACAGAAATAAATAAGATGGACTTGACGGTGTAAAAAGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGATG/CJTTCCTTTGCCAATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCAAGAAAAGGCCGCCGAAATATAGTGAGACTCA
WI-14284	55 C T	CCGCTGCTATT CCAGAT	GGTCTCTTTC ACCAATCTT	ATTTCAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACAC/CJTATTATGCCAT GCGGGAATAAAATGCTTATCCAGTGGGCGCTCCCTGATGCAATGA
WI-14288	85 G C	CCGCTGCTATT CCAGAT	GGTCTCTTTC ACCAATCTT	ATGACCAAGCAAGAACGCCCTGTTCTATATGAAGACAAACAGGTGGCCATCTTTGGTGGAGGGATA CCGCTGCTATTCCAGATG/CJAAAGATTGGTGGAGGAGACCATGACAGATGACAAACGG
WI-13522	33 C T	TGATGTAGTTA CCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGTAGTGTACCCCACTAATACAA/CJTGGAGAACCACTGACTTCAAAATATTATGAGAG AAAATTACTCCAGGGAAATTTTTCAGAGAAAGATAATA
WI-13529	42 T C	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCATCCACAAACATTTATTGAACAGTTACCA/CJTJAGCAAGAGAGTGAGAAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGGTTTATAGTCTAACAGGGGAACCAACCTCTC
WI-13859	84 G A	TTTACCA	GCTT	TTATTTGTCAGAAATTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTATG/AJACAAACAAAGTATATTCAGGAAAGGCACTCTAGAACTTGAGCA
WI-13536	29 T C	ACA TGAAGGATACAGAAAAAATCAGCGAAAGT/CJGAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAAGCTCCAGTTGCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52 G A	TTTATTTGTTGGTAGAAAACAGGCTCTTTAACACTGAATAAACATCTCAC/GAJAAGTGTGCTC CTAGATTACAAAAGTCAAAACCAATTTCCTTTGACCGCGGCCCTTGAATCTGACATTCAGATCAC CGTAATAGAAAACCAAGCT
WI-13477b	61 A G	TTAATACCTCT TTATGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTATTAATACCTCTTTGTTGGATAAAAGGACATGTTTTCATTAGCTTCTTCAAA/GJGAC AGAGAAATAAGATAAATTAACCTTAAAGAAATTAATAGAAAATTAAGGGAACATGTACCAAGGTGG TTTATAGACTCTCCCTCAGTT
WI-13477a	32 A G	AAGG	CAATG	TTTATAGACTCTCCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACITTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTCAGATTATAAAAAAT GTTGGGTACTTTTTCAGATTAATAATGTTTCTGAATGTGCACACTAGAAATATATGCAGAAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAATATTTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAATTTGJACCAAAAAATTAAGATTTTTCGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGACCAATGCAATCTAGAGACTGGGGA/CATGGAATCTAACTGGCGCAGAG AAATCAAGAGCCGATGTTGTAATCTGGGCGAGCTTCAAAATTTCTGCCCTCAAAACATTTTCAC CCAAITTTTTCATTATTGCC
WI-13857	28 A G	---	---	TCTGAGTTGATAAATGCTTTTCTGAA/CATGATACATTTTGGTATCTGGCACAATTAACCAAAATGT CTGCCAATTTTGTGTAGCTTTTCATACAGTACAGATTTTTCATTGATGTCCGCTCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCATGTTT GTAAA	GTTTAAAGTTCGACAGATGTGAATGGTTTACAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGT GTAAATGCC/TGTTTACAACATTTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T	---	---	TTAATCAGTCTGTGCAAGAGAAACAGGACTTGTATCAAGCTCCAGGCTCCAGGCTTCAACAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAAGGAATTTGGAAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T GAA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTTATCCAAAGATGGGAGCGCAITTTTCAATTTGCTTGAATGAGAAAGCTTTCATCTCCACTCTA GCTGCAGTAATACT/GTGCATCCCATCCACTCTTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
WI-15801a	24 G A	TTTATTCCAAG AATGGGAAGC	TCATTCAGGCC AATGAAAA TG	TCITTTTATCCAAAGATGGGAGCGTACAAATCTGTTCAACACTGGGCTGGACACTGCAGTGTATTCJAGGG GCTCGTATGAGACAGACGCTACAAATCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA GCAGGTGTGGGGAGGGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13783	59 T C	GCAGTGAT TCAATAAAGA	CCACACCTGC OCCCT	TTTITTTTGTGTGAGTTTGTCTTCAATAAAGAGGAGAAACAACTTATGACAAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCCCAACATGATATTTTCTTTTCCGAGGGCAAAAAAGA GAGTCTTCCAGAAACCTC
WI-13578	48 T A	AACC	GTC	TCCAAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATTTGGATGGCTGAGGGAG/GA GAACAGAGGAAAGCGCACTGGGGCTGGGACTGAAATATGACAGTGGATGTTAGGCTCTCTCTCTT GAGGTCCCT
WI-13789	62 G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	AAATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAACACAGATACAAAAAGC G/ATGCAACAAAAAGTACTGGGCAAGGACAAAAATATGCTAAGAAATTAGGCCAACACAGCTGC
WI-13594	66 G A	ATGATGAGC	CCTTTGGGCA GTACTTTT	

WI-15625	40	CT	GTTCCTCCACCTACTCCGGCAGAAAAAGGCATATTCAAC/TTGTCCCATACTAAATTTTGAATAA CCTAACTCTCCCTTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84	CGA	CCACACTGAA GACTCACCCAG	TCCCCACCCCA CCCT	GTCTCACTTTCTGTCTAGGCTGTAATTTTCAGTTTACAAGTTTCTATGTGATTTGTGGCCACACT GAAGACTCACAGAA/C/GJAGGGTGGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCTCT
WI-13600	28	GT	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACITTTAATGAGCCAGCATCCAT/GJCCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAACAAGAATACGGATTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89	GT	TCCATTCTGGA GACAATATTTA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAGAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCC CTTCCATTCTGGAGACAACACA/GJAAATCTATTAAATATTAATATTTGTCATGAGGTATGCACCT GCOCA
WI-13650	76	AT	AAAGATTAC AATATTTCACT TTTAAAAAC	CAGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAGATTTCACAATATTTCAC TTTTAAAAAC/ATTTAAAAAACTACTCTTCATATCTCTAGCCTGATGACTTAAAGATTACCGG
WI-14319	83	CTA	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAGC/TAACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAAT
WI-13528	80	AGA	CAATACATT GCATTTTCCTA AGAAAA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAACTCAATACATTTGCATTTTCCTAAAA AAAGAAAGACATTTT/AGTTTCAGAGAAATCTGTGTATCATGAGGAAAGCAGAAAAAATTT ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTTCCAGTGAAGTTCACTCTCTCACACT CTCTTCAAACTCGAATATCTTTTCT/ATGAGATGCTAGCTAGTACCACCTGCAACATCTCTCAA
WI-13909c	93	AT	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTTCCAGTGAAGTTCACTCTCTCACACT CTCTTCAAACCTC/GA/ATATCTTTTCAGAGATGCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	CA	ACAGAAAAAT TAAGAATCAA ACATCA	...	TTTTTATTGAATTCCTCAATGTAGCAAAATCACTTAAACAAATTTATAAAAGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC/ATATGGGAACCTTGAAAAAGGCGAGTGGAGCCAGTAAGTA
WI-14323a	78	CT	AGATAATGAA ACATCTGCGA	GCCTTTTCAAG GTCCCAT	TTTTTATTGAATTCCTCAATGTAGCAAAATCACTTAAACAAATTTATAAAAGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC/ATATGGGAACCTTGAAAAAGGCGAGTGGAGCCAGTAAGTA
WI-15389b	104	GA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCACACTT	AAAATTGACAAATCAACTAGCTGCTTTTGTGCTTTTGGAGACTACCATTTTCAAAATTTATGT AATACACTCATCCAGATAATGAACATCTGCGAAAA/GA/AGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 GA TC	AATCAACTAG CTGCTTTTGG	TTGAATAATG GTAGCTTCCA AA	AAAAATTGACAAATCAACTAGCTTTGCTTTTGTGCGAATTTGGAAGACTACCATTAATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAGTGTGGGAATCACTCATCTGTGTC
WI-15747	88 T C AGTGTT	TGCTTCATTT AAACTAAATTT	CATAATTCACC AAAGITTCATA TAATTT	TGTAATCTGCTTACAGTCTTTGCAAGACAGACATATGTTTTCGATAAAGATATAAATTTGCTTCAT TTTAACTAATTTAGTGTTTTCGTTTAAATATATGAACCTTTTGGTGAATATGAACCTGTACCAAAAC
WI-13752b	117 CT	AAGAAAAGCACATACATTTCCAGAAATTTTGGAAAAGTTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCGTTAAGTCTGGATATACCTTGGCTTGCACCTTTTACG GAGGGATTCGSGACAAC
WI-13752a	106 T C AGTGCTGA	CCTTCTCGTTA AGTGCTGA	COCTCOGTAA AGTGCTGA	AAGAAAAGCACATACATTTCCAGAAATTTTGGAAAAGTTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCGTTAAGTCTGGATATACCTTGGCTTGCACCTGTACCTTTTACG GAGGGATTCGSGACAAC
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTTCCAAACACACCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCAACCCCAATCAACAGTACATGATTACTTCTGGGTTTCCAGAAATCTGGATAC
WI-13744	115 CT AAACTGAA	TGGTGCTGAAC	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACAGTAAATGGAACCTTTCATGCAAGCTTTAGAT TTCCCTTGGCCAGCTAGGAGCTTGTGTATGGTGTGCTGACAAAACCTGAATCTGCTGTATCTTTC CTGATTTCT
WI-14081	68 CT	CCTTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGCCCGGTACATACCTTAT CTTAAACCATTTTCATCCACCATTTGTAAAAATCTCATCTTCTGGGCTGTGATACCTCAAAAACAGAT
WI-15719	69 A C CATTGAGC	ACCTTTGATC CATTGAGC	TGACTTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAAACACTACACACTGAATATACTGAATTAACCTATTCAACCTTTTCATCCATTCAG CTAATTTAAACTCTTGGCAAGTATCATGAACCTTACGAAGAGGAGATAGAGATCTGATC CTAATTTAAACTCTTGGCAAGTATCATGAACCTTACGAAGAGGAGATAGAGATCTGATC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT ATT	TAATCCCATCAATCTAAATCAACATCACTAGATCAAAAGAAAGTACCACAGTATGCTTTATTTTGGCA GGTATTAAATGGTCTCTAAATCGATACATCCAAACTTTTCTAGTTAGCAGCAAGCATCAGTTCTTTC
WI-15736a	27 GT CACA	ATTTATTCAC ATTAACCTTG CACA	GTCTTTTGATA TGCTGCTTAGT TTT	GGATTTTATTCACATTAACCTTGCACAGTGTAGCAAAAAAATCAAAACATATAAAGTAAAGCCACA TATCAAAAGAACATATACATAGAGATTGAATTTCTCAATAGCATGGAAGGTATTTCCATAAATA TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC
WI-13785d	72 GA	AAGTGCCTGATAGTACACATAGCTGTCAACACACAGTG
WI-13785c	56 A C	TCAAACTGCACACTATAAAAGTCTTTAAATGCAGCAGGAGATGTGAAGAGCTGCAAAATG AACAAAGTGGTAGTACACATAGCTGTCAACACACAGTG

WI-13785b	40 C G ...	AAAAGTGCAC ACTATAAAG	... TGTTGTGACAG CTATGTGTCAC	TCAAACTGCACACTATAAAAGTGCCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTGCACACACAGTG
WI-13785a	27 T C T G C T T	GGATTTTACAT TCAGCCTAGAT	T TTTGTACT	TCAAACTGCACACTATAAAAGTGCCTTT[C/G]AAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTGGTAGTGACACATAGCTGTGCACACACACAGTG
WI-13793	88 C G A T A G G	TTCTCACCCCT TTCTTCTCTC	AGAATGGGCTC TTAACCCTTGA	AGAAACCAAGTATATCATAGGCAAAATAAAATAGTTTTACCCCATTTGATACACATAAAGGGATTT TACATTGACCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATATAAATCTATGACTTG
WI-13794	52 A G T T C T T C T C	TTCTCACCCCT TTCTTCTCTC	AGAATGGGCTC TTAACCCTTGA	TAGTCTCTACAAATTCCTCAATCCATTTCTCTCACCCCTTTCTTCTCTGAGJTACAAGGTTAAGA GCCCATCTCTCAACAAACAAACAAACATAGAGCAAT
WI-15729	35 A G T G T A G A C T G C	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTG[C/G]GGCCTTTAGAAAAGAGCTGAGACTGAA AAGTCTGTCTGACTTCCAGGAGGGTAAGTCCCTGTTTGACGCCCGGGCTGCTCATTTGTA
WI-13424	66 G A C	TGAGGTTTTTC ACCCTATCTT	TTTTTCTCCOC AGGGTCTA	GTCCCTTGACACAAGTCTCCCAACTGGTTTGGAGTTTTTCCCTTCTGAGGTTTTTACCCCTATTCTC[G/A] ITAGACCCCTGGGGAGAAAACACATGTGTAAAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C A A T T	TCATTATAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAGGTCAGAGGCAATTT[C/G]AGATCCAGATTCAGCTTGTCTCATATAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAACTGACATTTCTTGAAGCAGAA
WI-13446	22 C C T C A C T C A T C A	GCCATGTTCTT TCACACTCATCA	AAGGGAATCA AATCAGAAG	TGCCATGTCTTTTCACTCATCAG[C/G]CCTCTCTGATTTTGAATCCCTTTCTGCTCTGTAATTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTGAATTTCTGTTTTTGAAGTAGTAGAGCCCTTTTACTTTTTT CTGACTGSCCTAAT
WI-13725	56 A C T G G G T G C C	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGAAATGTCACTTACACATGGTGAGCACATATGGGTGC[C/G]GCCCGAG ACAGCAGGATAAGTTTCAACAACTTGACAGGCAGGTTAGAGCAAGGCATGGTTTCAAGATG
WI-15702d	107 T C ...		---	CAAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAGGGGGTAAAGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAAAT[C/G]ACTAATGGGTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ...		---	CAAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAGGGGGTAAAGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/G]TGTAAACAATACTAATGGGTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ...		---	CAAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAGGGGGTAAAGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/G]TGTAAACAATACTAATGGGTCTTTGAACAAATAGTTT TGA

WI-15702a	48 GC	AACAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTCAAAG[G/C]GGGGTAAAGGGTG AGGAAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAAAGGGTTCTTTGAACAAATAGTTT TGA
WI-13831b	113 TC		---	TTTTTTTTTATGGATGGACTGTACATGTTTATTAGCGAAGGTGACITGGAAAAGGAGATTTCACAT ACTTCCACTGTATCCTCCGGGTAAGTTTCTCTCTCTGTAGAT/C[GTCTCCATGTTACAGTCAAC TATAAACACATGGCTCA
WI-13831a	56 GC		---	TTTTTTTTTATGGATGGACTGTACATGTTTATTAGCGAAGGTGACITGGAAA[G/C]GAGATTCA CATACTCCACTGTATCCTCCGGGTAAGTTTCTCTCTCTGTAGATGTCTCCATGTTACAGTCAAC TATAAACACATGGCTCA
WI-13808	82 GA		---	TGATTGAGCTTAGAAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAAGTCCAGGT[G/A] CCATTAGCATGCTGTGAATGCAAGGAAAAGCTTAAAAAATTTTTTAAAGGGTGACTCCAGTAAA CAT
WI-14372	86 AG		---	CACATTTTCAGCAACAAATCGAGGTGCAACACAGGGTTTATTTCACATTAATATTAACTGGATT TTTGTCAAATAATAGGGA[G/G]TCTCTTTAAATAACCATCTCCTCATTCTATGGCCAGT AGGCTGTTTTTTGAGGCTTGAGGCCCAACATGACAACTGTAAGACTGTAAACATGGTGTGAGTT ATGAGCTAGGAACCCCTGGAGCAAAACCAAGACATATACATCATCTCCCACCTCCCAACGCCCTTT ACTTTCAGCCCTCTGCA
WI-14078	61 CT	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAGAACCACATGGTGTATCAAGAAGTAAATAGGAAGAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAAGGACTTTAGATGGTCACG
WI-14083	47 CT	AGACTTGAGA GCTTAAACA TACACT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACACACACT[C/T]ATTTGTTATTTACAG CTCAGTAGTTTAGAGGTCCAGTAGGCTTGCTGAGTTGTTGCTTTAAGGTCTTACAAGGCCAA
WI-14085	31 AG	CATTATTTTC ATGTGTAAGA AGAAAAA	CAGTCATGTC ACGTGCTAGTT	TGCAATTTTTCATGTGTAGAAAGAAAAAC[A/G]TAACCTAGCACGTGACATGCACTGCGATGATAC ACGGCTCAGCACGAGGCTTAAAGTCAGAAGTGAGTGAAACAAATAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCGCTTT
WI-12169	121 GC	AATAAACTT CCTATTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTGGCAATTTTATTTCCTACTATCAAGAAGTACAAAATATTTTGTTCATTCTAAA TTTTCCACTTTATTGCTAAGTTATAAATAAAACTTCTCTATTCTTTGCTT[G/C]TTTTTCTTCA CCTCAGAACCCCTTA
WI-15705	50 AG	GGAGGGAGAT TTTAGACTGA GATC	AGCTGTAGTGG TCAAATACTCT AGAA	TTGTTTTTATTGGGGAGAAATGAAGGAGGGAGATTTTAGACTGAATC[A/G]TCTAGAGTATTT GACGACTACAGCTCCTCTCTCTTTGACTACGGAGACCCTGCTTATAGCCCCCAACAGGAATCTCTCA TCTCGGGTTGCGAGACAG

WI-14379	102	C T	TCTATTAA GGGTATGTCA CAAC	ATCATCTGTT TGAGGTTGACA	TTATGCTGTTGTTTCTACTGGTGGTGGCTGCTCACTAATATCCAACTCTAGTATGATTTCTTT TACTTGTCTATTACAGGGTTATGTACACCC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCCACTTAACAAGAGGACACTGCAGAGGCTTATGTACA ACAGTGTCCCGAGGCTGCGCAGGACTGCCACTCCTCCAAAATTTCTTTGAGCAGAG
WI-14102	22	C A	ACCGCAGAGCTGCTGTATTAAAGACAGCGTCTGGATCTCGAGGGGCTGGAGCCAGCTGC AGTGGGGCTCCGGCACTGCTCTCTCGAGGACTCTTCCACCAACCCC
WI-15937	24	A G A	CGCAGAGCTG CTGTATTAA GA	GCAGAGATCCA GACGCTGT	TGAAACTGAAACGATTTCCTCCA/CACACCGGTAGAACTTAAAGCCGCGAAAGACTCACACCC ACCACTAGCGCGGAAAGAAAGTTTCAGGTGATACAAGATGCTCTGCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	AAACTGAAAC GTATTCTCC CA	GGCCTTTAAGT TTCTACGGTG	ATGTTTATGATCAATCCAAACATACAGTACAGGGAGGTGAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGGTTAACTAAGCC/CAGTATTATTCAAAATGTGTTCAAAATACTCAGCCAGAT CACCAAGCTCAGTCACTAC
WI-14124	92	A G	GACAAAGAGCAGTTTCTGTAGTTCCAGAGGGCCAGCAGTATCAGAACGGTGGTTTGACCT GCATAGATTTTTCAGCACTA/C/TGTGGCCATGCCATTCTGTAAAGTGAAATTAATGAACA
WI-14125	88	C T	CATAGATTTT	GOCAC	GTATTTTCTCAGAGTTCTGGAGTTAGAGTCTGAGATGAGGATATCAGCAGCATGGTTAGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGTTTACAT[C/A]GCCCAAGAGAC AGAACAGCTCTCTGGT
WI-14136	120	G A	ATGCTTCACA	CTGTTCTGTC TCTTTGGC	TTGTTGTCGCCACAGAAAGCT[C/N]ATGTTCTATGTTATGTCACCTGTACATACTGTAAACAAGACT GCATTAATATGTTTCTTATGATTGTTTCAATG
WI-14138	23	C T	TGTTGGACCA GAAAGCT	GTGACATAACA TAGAACA	GGCAGGTTATTCTAATAATTTCAAACTTGGAGCAACCAAGATGCTCTCAGTAGTAGTATTCA GACAACTG/AATATTACTTAGCCTAAAGAAATAGCTATCAAGTCATGAAAGACATGCAGG AACCITTAATGGATATTACT
WI-13551	74	G A	GACAATC	TAATATT	TTTTTAAAGAGTCTCTCAGATCATTTATATTGTTATGTCACACAACTTTTTAACTC/C/TGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTCTTTTGGATAGAAGCCCTCTTTCAGAAATCA CCTCC
WI-15953b	59	C T	TTTTTAAAGAGTCTCTCAGATCATTTGTTATATTGTTATGTCACACAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTCTTTTGGATAGAAGCCCTCTTTCAGAAATCA CCTCC
WI-15953a	26	T G A T	A	A	TTTTTAAAGAGTCTCTCAGATCATTTGTTATATTGTTATGTCACACAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTCTTTTGGATAGAAGCCCTCTTTCAGAAATCA CCTCC

p.

WI-16002	59 T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCTC TTTGACTTTT	CCACATTTTAAACCTATGACTGGTCAATGATAACATAAAATGATCATGAGAAATTTCA/T/CJGTTA AAAGTCAAGAGAGATGGCTAATGCATGCTGGCT
WI-15361b	101 A G A	CCACITTGAC TCAAGTCATC AAA	CTTTGTGCTA AAA	GTGGAATTTTATTAAGCCATCAAAATTTTCTTCACACTCAATACTGTGAAACAACAAGATAACACAT CTTCTGTCTCCTCCACTTGAAGTCAAGTCAATCAAGTTTAGGCACAAAGTTTAGTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73 T C	GCGTTTGACTT GTGCGG	TCCCACTGCT OCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAATTTGTTTATTCAAACTTCTAGCGTTTGACTT GTGCGGT/CJGTACTCAAAATGGGGGCGAGTGGGAGGGGAGATTGCAACAGAGTTTACTACTG CAA
WI-12535	50 A T T A T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCTTAACATTTATTTAGGTGGTACTAGAGAGGTGTAGGTGTAGATATTA/TCTTCTCTCTCTC GTGGAGCTTACTGAAGACAGATCGCGTTCTTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G A G G G A A	AAAGGCACAC GGGAA	CTCAGCTGOC TTGACC	TTCCATTCAATGCTTGGCTTTACCAATTTTATAGCTATTGGAGGCGAGAAAGGGAAATTTTGGC CCAGAAACCATGAGATTGGTGAGAAAGGCACACGGGAA/GA/GGGTCAAGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C	ACACAATATAATCCATT/CJGAGTGTATTAAACCTATTGTTGTTTAGAACCAACAAACTAG AAGAAAACATTTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52 T A C T A C C C T G T	ACCCACCACA CTACCTGT	GAGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCCTGTT/AJAAAACTTTAAC ATTGTGATGCCCTCTGCATCAATTTTAGAAAACAAGAAACACACACTGAAGGCCCCCATGTA
WI-14816	29 A T	AGTTAAAAAAATCGAGTCAAGATTATTA/TAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAATGCAATTTATTTTGATCCCAAGCCCTGAAACATGAAAAATATTACTAAAGGAATGTTG ATTACCAAGTACGACTTC
WI-12542c	71 G T	CCGTGTTTCATTGAAGGCTATTAGGCAACCTGAACATTTAAATGTCCATCCATGTGAGGCTCTAGATC ATG/GTTAGGTGATTGATACAATACGATCCATAA
WI-12542b	70 G T	CCGTGTTTCATTGAAGGCTATTAGGCAACCTGAACATTTAAATGTCCATCCATGTGAGGCTCTAGATC ATG/GTTAGGTGATTGATACAATACGATCCATAA
WI-12542a	45 C T T T T A A A	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAACCTGAACATTTAAATGTCCATCCATGTGAGGCTCTAG ATCATGGTAGGTGATTGATACAATACGATCCATAA
WI-12173	57 C T C A A A A A	GGATACAGCA GTAAAGAATA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTTAGAAAACCTGGGGATACAGCAGTAAAGAAATACAAAAATCCTGCTGCTTATA GAGCATACATTTCTAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---	TGGTGACAG GAAAATACTT	TTTGTGCTA CTTTTACAAA CTTT	---	TCTTTGAGGATAGAGACAGAGTGTTC/GTGTGATTTCCTGGTTTCAGTTTGGTTGTCTCAT GGTTTTGTTTTTGCCTAATTTGCCACCTTATAAAAGCAGTGCACCCAGAGCGAG
WI-14856	60 A T AA				ACATTCCTTATGATAGCAACAACCTAAATATGATGGATGGTGAACACGGAAAACTTAAATATTA AGTTTGTAAGAGTAGCAACAACAAATGAGTATATCTATAAGTGATAGGATGTATATGAAAAA GGCTATAAAAGCTCCAAA
WI-14863	61 G A ---			---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAGGGCAAAATATTTTGTCTG/GA/JAG TTAATAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACTATTAATGATGCCACT ACCTGGC
WI-14867	46 T C A	GACATCCAA GGCTCTCTAAC	TGGGCTGCAG ACACTC		TTTAAATTAACGTAAAAAGGACAGACATTCOAAGGCTCTTAACAT/C/GAGTGTCTGCAGCCCCA TTGGCTTTGAGATGTGAATGTGTAAOCCAGGGTGA
WI-14733	98 G A A	CCAAATTGAC AGATATCTGC	GATGAGGTCAG GCCATTTATT		ACGGAGTGTCTCTGATGTATCTTGTCAAAAATGTTTGCCTGATTCATCAATGAAAGAACAAAT AGAAAAATCCAAATGACAGATATCTGCA/GA/AAATAAATGGCTGACCTCATCAAAAACATCA ATGTCATGAACAAACAAAA
WI-14898b	79 A C ---			---	TTTTGTACCTATCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAAGGTGCCACTAAGGAAA ACTTCTCCAT/C/JAAGCTGCCTGTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGCTCAT GCCTGTGTCTGTCT
WI-14898a	50 A C CA	CATGTACAGG AAGAGTTGTCT	AAGTTTCCCT AGTGGCACCT		TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATA/JC/JAGGTGCCACTAAGG AAACCTTCTCCATAAAGCTGCCTGTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGCTCAT TGCTGTGTCTGTCT
WI-14907	48 G A GGACTCTGAC	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT		TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/GA/JATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGGCACACCCATCAATCAGTGACTCCTGCACAGGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTGGT	CAAACCCAGGA AAAGGACCTT		CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAGTTCTGTTG/GA/JAAGGTCTCTTTTC CTGTTTGCAGACAGATACCTTGTGTATCTCTACATGGCAGAGAAAGAGAGGAAGTAATCT
WI-14913	88 C A ---			---	CTGATGCTTTGACATCTGGGCAATGTCTGTCTCTAGAGAGACTACTTCTCTGGACCCAGCCAAATTC TAGTGATAGTAGAGGACTCA/C/JCCTGCACGTCACCTTTTATATACAGATCAACCAATCCAAAAAC CTACACCTCCAAOCCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCOAGGA CAATAAATTC		ATTTCTTGTATGGTGTCTGTAAGCCCTGTGAAGTCATGCACATCTGGACACAGTTTTTCTCTAGCA/G C/GAATTTATGTCTCTGGCTGTGATGGCTTTTCACAGC
WI-14926	49 T C ---				GTTAATTTCAAAATGACACATCCAGATTGAATGGGCACCTTAGCGAAT/C/JACTTGTGGACCACA AGACTGTCTGAGAACATGTTCAAGACAGATTTTCAAAATAAAAAATTTCTTAAATCAGGTCCA

WI-16083	89	C T	ATGTTTAAACA CAACATATC AAGGAT	TGAAAAGATT CCAGCC	GCATCTTTATACACAGAACTCATTTATGTCCTTAATCATGTTTAAATATAATAAGCATGTT TAACACAACATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55	C T	GGAGGATOC CTCATGGAT	CACAACCAAC AATACCG	CAGTTCTGTGTTCTGGAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTGGTTGGTGATTGGGGAGCAAGGAGGAGCAA
WI-14946	47	T C	TCAATCTGAAGGTGTCAAAGTGTCTATTGCCCCCAGACATAACAT[C/T]CTCTAAATCATCTCTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATTACACACAGTACTTTATGAAAAGGATT
WI-15987b	80	A G	ACATTAAACACAGCAAAATTAAGGGTCCCAACGAGTTGGTAGTCCCTCCACTATGTGAGGACAC TAAGAAGATGGTCAG[C/T]CTATGAACCAAGTCCGGTCCCATGCTTTAAACCTCTCAGC
WI-15987a	32	C T	CACAATTAAA GGGTCCCAA	GGAAGGCACTA CCAACTC	ACATTAAACACAGCAAAATTAAGGGTCCCAAC[C/T]GAGGTTGGTAGTCCCTCCACTATGTGAGGA CACTAAGAAGATGGTCATCTATGAACCAAGTCCGGTCCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T C G	AGGGAACCTG CTAACTTGTC	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTATTGCCGTTCTTCCAGGAACAGGGAACCTGCTAACTGTCTCAGT[C/T]CCAAACA ACTGATGTAAGATCATCTCTGACCATAGCAACCTGTAGGCTTGTCTCCCTCCAGCTGA
WI-16100	52	A G	CAAAAAGCTA TTTTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[C/T]GTAATATACTG TTTTCTGACATTCCTGTTATCAACTCTCTCTGAAAATC
WI-14958	83	A G	AATAATTTAT CTCTTCTTTT CAAGCG	AATGCATTCAT TTGGGTTT	GTGATTGATCTGTAATTATTTGGGATTATTTTCAACTCTAAATTCCAAGATGAAAATATTTATCT CTTCTTTTCAAGG[C/T]G/AAAAAACCCAAATGAATGCAATTTTTCAGTTTCTCCAGGCTTTTGAAGTGC AGCAGAAAAATTCAGGA
WI-14976	35	C T	GTGATTGCT TCGTTCAAAG AGC	TCAAACTAAAT CTTCCATCTA AGC	TATTTTAAATTTGGTTGATTGCTTCTGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTGGGGTAGGCTCAGCGGCATAGTGGCCACAAGATGCCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	G T	TCAGTGGTGT TATTGGATTT ATAA	CACCTCTGACA TAATACCTAGC ATAA	TAATTGATTCAAGTGGTTTATTTGGATTTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGAGAT AAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTCAAGGAAGTTTTTGA GAGCTCACAAA
WI-14982	80	C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTCCCT	TGATTACATTTTAAATCATGCCTACAGCCCATCTAAGCCAAATTCAAACACCACTCTGCAATTA AATGAAGCTTGCAG[C/T]AGGAAAGCTGAGCACATAGACCCCACTGATCGGAAAGAAACGTA AAATCTCTCTTTCACACACAGATGAACCTTTAATAAATACAAATGCACTGAAATGCTCTCTTGA TTTCTCTTATTCAGTTTAGGCTCAAAATGGGCTCTCTCAAGGGTGGACCTCAAGGCGCCAGTT
WI-15000	90	G A	GACAGAAAA GACTCAGACT GTCTAA	GTCTTAGTTC TGCAAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGATTTGAAGGTATAGAAATAAACAGATGATAGACAG AAAAAGACTCAGACTGTCTAAGTATGATGAGTTTGTGCAAGTATAGAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACCTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACCTTCATGTACCTATGAATAA G/AJACAGGTAGGGAATATGTCAGTGGCAACAGAGGACTCACACCTGTGCATAGACAGCACCC
WI-14683	91	A T	AAGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTCAGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACACA/ATCAAAAAAACACTGGGACATGCCCTGAAATTCAAAGT TGGAGTTGTAAGAACTAC
WI-13470	100	C A	CCTGCCCTTAT ATTGGAATTC T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAAITTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCAAGTGAGGAAGCC AGGGCACCTCAGCCCTC
WI-14712	38	T A	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCAT/ATCTCACAATACCATATACAACATACT TTCAATCACAACCTCAATATAAATAACCTACAAAATCACATTGC
WI-13712	40	C T	TTTACTTTTGT GTCAATTTTAT CTCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTTACTTTGTTGTGCTATTTTCTATTCTATG/CJATTATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATGGCAATATGCAATATAATATTGTGTGTTGTTAAATTTATGCAT
WI-16163	35	C T	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACCTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA/C/ATTTGTAAGTTAATGTAAATGGCAGCAT GCCAAAAGTTTAAGAGGACTATTTCTTTAAACAAGACAGTGTCTGACATTTATTTCCAGGT
WI-13453	88	T A	AATGCACAAA ATCTGTCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGCAATTTGAGTGTCTTATATATTGGGAATTCGAGTGATTTAAACATTTGTACAAAT GCACAAAATCTTGCTCTCTG/ATGCTAGAAAAGAGATGTAATAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTTGCCAT
WI-16167	58	T C	CGCACTCTAA ATTAGAGATA GATTTT	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTCTGATATACATTT/CJCATCTT ATTACCCACGAGCACACACACGACAGTAGAACAGTCCACACCTGATAAATTCACAAGATG
WI-14482	17	G A	GCAGAACCAATTAATAAG/AJAACTGCAAGTTTCCCAAGAACTCTCGAACCCATAGTGCCCTAAT GCCCTTTAAATCGACTACTAAAGGAGAGAGATAAAGGAGCTGCTGTGATGTGACAGTCACTGGT TGATGTTCTCAAAAGACATGTTGGCAGATAGCCAGGCCACTATGTATTCCTCCAGTATCATGTAC
WI-15069	81	T C	GCACATAAAAAAAT/CJGTGTGCTGCTGCTGTGAGTGAACCATTTGCTTTAAGATAAA ATCTGGTATTGTGTATCCCAACAGTATACAGAACTACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTGGC/AJCTCTCTCTCAAAATGCACACAATTAAGACG
WI-16156	97	A C	TGAAGATTAA CCAGAGTCCG GCAGCAAGAT TACATCAGTA	AATGTGTGCA TTTTGAAGAGA CTCCAATAGC CTAGAGTATAG	ATCTGGTATTGTGTATCCCAACAGTATACAGAACTACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTGGC/AJCTCTCTCTCAAAATGCACACAATTAAGACG
WI-15012	59	G T	ATGT	TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTCAITTTGAAGCTTTG/TJACCT TACTACTCTAGGCTATTTGGAGTGTCCCCAC

WI-15100	74	G A	GTCAACATGTT ATATTTCCTT TAAGAC	TCATTACAGCAAGCAAAATACCAATATTTCCAAATAAAGCAAAATTTGGAACAGACTGGA GTGAGAAQ/GA/GGTTCCACCACCAAGCCCTCAAGACAGATGACCGGCGCTGGTCTGGGGT GCATTCTAGTGGACTTAT
WI-14492	92	A T	AATTACT	...	CCCTTATTTTC CCAAATATAA TAAGAC	TGGTACAGATGTTTAAATACAGCAGGGCAGTGATTCAGTTAAATATAAATTTAAACCTTTATTT CCCAATATAAAATTAATAATTAATGTTCTTAAAGAAATATAACATGTTGACAGCTTT TCTTTAAATTTATCGGAATCCAGGACACAAAGAAACACCCAAACCATGAGAGACAGAAG ACGAGACACAACTCTCCCCAC/TG/SCCTCCCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-12002c	89	T C	TCCTTAAATTTATCGGAATCCAGGACACAAAGAAACACCCAAACCATGAGAGACAGAAG AC/GA/JAGACACAACCTCTCCCCACTGCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-12002b	68	G A	TCCTTAAATTTATCGGAATCCAGGACACAA/GA/JAGAAACACCCAAACCATGAGAGACAG AAGACGAGACACAACCTCTCCCCACTGCTCTAGAGTGGGACAAAGTGGGGTGAGAC AG
WI-12002a	30	C G	GGACAA	...	TCGGAATCCA GGACAA	TTTTCAATTTATTTCCAGAAAGAAATCACAATTCAGTAACAACATACATATAGAATTAACATTTG TCTGGAATGGAGCCCTAGTTGCAGTA/C/TGTGTCAATAATAAATTTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-15116	96	C T	GTTCAGTAA	...	GGGAGCCCTA GTTCAGTAA	GCAAAAGCAAAAGCTATGGAGGCTAAAGGAATGGAA/C/TGTGTGGTGGTGGTGGTGGTGGT GCTTGTGTGCATGGAGAGAAAGTCTTCTGCTCCATGCAGGGCGTCACATATTTTAAGTGCACATAAT TTGGCAAACTGTCATTC
WI-12578	37	C T	AATGGGAA	...	TCAAGCGACCA CAAACAC	ATTTACAGTTGGCCAAAGATCTCCCTTATGTTGGCATTCGA/JAGACACTGCACATTTCTGAGTTA GAAAAATGTAGTCTTAATAGCCCTTAATGTGTAGCAAGGCAAAATACCATTTCTAA CCTTGTCTCTGAAGTGGGACAGATGTAATAATTTTGAATCTGATGCAGGTGAGGTATGGC TTTGAATCAAAATGGG/GC/TGACTTTTCCCTCTGGTGGGAAACCTCTGTGAGGGTTTGGCA
WI-15215	84	G C	TCAAATGGG	...	CCAAAGGGGA AAAAGTCA	AGGAAAGAGTGGTAAAGCAAAAGGCGATCATTTGGATGGAATGATTGTGTCACGAGCACTTGAGGAC CTAGAAAGCAAAAC/TG/GAGTGATTATGCCAATCAAAATGCAAGGTTGGAGATATGCTAAAA AATTTGCTAGTGCAAATGGACCCAGAAATTTGGAAGGGCTATGTAAGTACACAGATATGACACACCAC AGCCATGTCACTGTACAGATCCCTCTGTGCAATTCAGCTTTCTTAAAAACATCAAGGCTGCA
WI-15152	51	G A	TTTGATTGGCA TAATCACTCC	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTACAGACAGATAAATAGGATG/C/TGTCTGTTT GCCCTTAAGCAATTTACAACTCAC.TGGGGAAGAAACAGACATGCAAAACAGAGATAAACACACAT
WI-15123	55	C T	TAGGATG	...	TTGCTAAGGG CAACAGAC	

WI-15182	49 C A	GCACAACCCAG GGCAAAATA GGGCGCTGGC GGCTCTGGC	GCATGGGTTAA TCCAGCA ACTTATCGTC AGGCAGAGTAG	GAGACTGCCCTGTGACACAACCTAGCTAGCTGCACAACCCAGGGCAAAATAC/AJTGCTGGATTAAACCC ATGCTAATGGGTACCTTTATTTAGTAATCATGGGTCCTCATAGCATGGTCCAGATCCG GTGGACCTCTACAAGTACCATGGCCCTTGGCACTATGTC/TCTACTCTGCCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT TCAAGTGGTAATAGCAATTTAGATTTCTGCTTTGATTC/TCTGCTACGTAAGCATGTAAAGACT ACAACATTACGACCCATCTCTCAAGAGGAAGTCTGTTATTTATGAAAAACATTTTGTTCATTCAGAT T
WI-12601	42 T C	TGAT	TAGAC	ATGTTGAGAGTAATATGCCCTACATATTTAGTGTAAAGTACACCCAGATATTTTGGGGAGAAGAG TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAAATAT/TGCCAGTTTAAACCATTTTCAAGAGT CAGTGTGATGACATTTTCATGGGAAAGATTGTGCAATTTGCAATAAACACCATCATTC/TCTCTGAG TCCACAGATAAGTCCCGGAGAGGGCTTCCCTCTCTCTGCTGGGTGACGTTCCAGGCGAGT GAAGCTTTTCTGGAATG
WI-14510	104 A T	AA	TAACTGGCA	ATGAGTTTATAAAGTGGACAGCGCATCATATGAACTGTCTAGCAGTATTATTC/TCTGCTATTAGCTA TGTTTACAAATTTGCTCTGAAGGGGTCTAGATGTGTACACCCCGAGAAAGTGGTATTCCTGA TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTTTCTTGTAAATAATCTCTGGCTTTCTCTGGCTGG TGAGGAGGACAGGCTGGGCTCTCAGGTATCCAGTGTCCAGTGGTCCGCGCATCTGTCTCCCTCCACTCCCGAG CCACATCTCTGGCTCT
WI-15239	57 T C A	GA	GTGGACTCAGG	CTGTCCGGGGAAGACACCGTGCAAATGC/TAAAGTGCACCTGAGGAGAGGGGAGGCTCTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGCGATTCATCCAGGGAGATCTGC TCCCTCAGATTGTGAAATGCTAGTGGCATTAGGATGC/TAAAGTGCACCTGAGGAGAGGGGAGGCTCTGTGACTC AACCGATTTAATTCACCTACTACTCTAGTGTAGTGTCTTACTTTGGATTATCTCACTTAAACCCACA ATGAGAGGTAAAGTGTCAACAGTAAAGCTTAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC/G TCCATTTAGGCTTTGTTGTTCCATTAGAGAGCAGGAGAGGAAATTTAGCATAAATCTT TTTATAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTAATAGTGGAAACAAAGGATGAAGCT AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGAAATTA TCCCTG
WI-12648	41 A G	TAAGGATGC	AGTGGACATCC	AGGTTTAAATGGACTCACAGTTCCATGTGGCTGGGAGGCTTCACAAATCATGGTGGAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAAATGAGAGC TATTTGAGTATTTTCATCCATGGGCTCTCACTCCCTATACATCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCAAGACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATCT/TAACTCCATGT GGGAGTTTTCATAATAA
WI-12684	64 G T	ACAGCTGTGC	GATGTGA	ATGAGAGGTAAAGAGGTGACACAGCGGACACTGTCTAATAGTGGAAACAAAGGATGAAGCT TTTATAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTAATAGTGGAAACAAAGGATGAAGCT AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGAAATTA TCCCTG
WI-15260	75 G A	GA	AGCTTGC	AGGTTTAAATGGACTCACAGTTCCATGTGGCTGGGAGGCTTCACAAATCATGGTGGAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAAATGAGAGC TATTTGAGTATTTTCATCCATGGGCTCTCACTCCCTATACATCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCAAGACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATCT/TAACTCCATGT GGGAGTTTTCATAATAA
WI-15325	39 T C	GAGGC	GATGTGA	ATGAGAGGTAAAGAGGTGACACAGCGGACACTGTCTAATAGTGGAAACAAAGGATGAAGCT TTTATAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTAATAGTGGAAACAAAGGATGAAGCT AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGAAATTA TCCCTG
WI-13936	123 C T C	ATAGCCCTAT	ATAGCCCTAT	ATGAGAGGTAAAGAGGTGACACAGCGGACACTGTCTAATAGTGGAAACAAAGGATGAAGCT TTTATAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTAATAGTGGAAACAAAGGATGAAGCT AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGAAATTA TCCCTG

WI-6375	28 A	GGTTATGCA TATGGAATC	AATGTGAGATC TTATTCTAAC CTTTT	AAGTTTATTGCATATGAAATCAATAGAGTATCTTTACAAAAAGGTTAGAATAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAAT/AJGCAACTGACAGTTTGAAG GACACCAAGACAATAGGCT
WI-6409b	112 T A	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACATATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAGACAATAGGCT
WI-6409a	73 A T	CTAATATACTCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTCAATATAGTTACTTAA CAGCTAAATAATAAGGGTGTATTAACTTACTTACAGAGTCACTAAATATGGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGCTGAAGCTG/TTATCAACCTTCCCTAAGCATCTGTCTGTGTCGG CAGC
WI-6523	165 G T	GCTAATCCAGT AGAGACTGAA GCTG	AGATGCTTAGG GAAGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTCTCTCTTTTCACACAACCTTTTCCCTGAGA ACTGTCCAGTCAAGTGGACCTTCAACAACACAGACGCTAAACCTCTGAGAGAAAAC/C/GJCTG ACTTTCAGAAAGCATAAAGCTGAGAAAA
WI-6554	195 C G	ATTGTAATTAATTTACATGGCCTATTATTAAAGGACATTTGTAAATGTTCCACTTTGTTTAAA /C/TJAAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTACAAGTTTGAAAAATGGCG
WI-6558b	68 C T	ATTGTAATTAATTTACATGGCCTATTATTAAAGGACATTTGTAAATGTTCCACTTTGTTT AAACAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTACAAGTTTGAAAAATGGCG
WI-6558a	42 G C	AACCAACAAACCTAAGAAATGGGAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATAT/CJAGCAATGGATGTGTGTCAGAACATCTGCCAATAAAGCTTTTAAGAAAAAGGA ACTCAATGAAGTACTGTATATAAACAAGGAGCTCACAGAGGGATGTAAAGATTATGGAAGAT ATCGTGAAGCCAAAC
WI-6629	75 T C	TCTTTTCAGAG AATAAAAGTT GTGATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAAATCAATCAATCAAACTCCAGCTGTTCTCTGCTTTT TTACTTAGCAAAAGGAAACCTTAGTAATGCTACTTGACACAAGAAAGTCAATTTCTCAAGCACA T/CJACCCAAACTTGAAGGTGATTAAGCCCAATAATATGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGGTTATTTTGTGTTGCTGCAAT
WI-6644	134 T C	TGCTAAACACCACTATTAAAGGAGAGTACTAGGAAAACTACCAAAACACAGCATGTGAAACAGT TGGGACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC/CJTGCTAATACACTGCAATATTTTA TGTTTAGCAAAATTATAGCTGGTGTGTATTAACCAAGAGCGGTATCTGG
WI-6690b	106 C T	AGCCACAGC	TAGCC	

WI-5690a	28 T	AAACACACC ATTATTAAAGG T C A G A G	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACTATTATTAGGAGAGT/CJACTAGGAAAACCTACCAACACAGCATGTGAAAC AGTTGGGACGGTGGTAAAGGGGACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTAGCAATATTAGCTGGTCTGTATTAACCAAGAGCGGTATCTGG
WI-6770	53 A	CAAAACCCAA AACATCACACA G C A T C T C C A AAACCAAGA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTATGACACAGATCTTCCCAAAGTAATCCAAACCCCAACATCACAA/GJAATATTTCAT ACTATTATACACTCCAAAGCAAAATACITCAACTGCAATCC
WI-6886	151 A	GATCTAACAG CTGCAGAATG	CCTTGTAAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTTCAGCAATACAGTACAGTAACTCTGACCAAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTTTCACTTTAAACATGGTAACTCCCAAGCATTTCT TCCAAAACAAAGAAAT/GJAACATTGGGAATAGTCACITACAAGGAC
WI-6761	32 C	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG/CJACTCTTCCCTCCAGCTTTTGTGAACAAAC AATCTCTCTAAGGCATCAGAAAGCAGCTGAGTGCAAAATGGGTGTTCCAGGTACAAGGTCTC
WI-6844	225 T			TAAATACTGCCAAGTACGATTTACGCTCCACTTTCATCATTTAAACAAAGGGTATTTCTCCTTG GTATTTCAATGATGCATTATACATTAACGAAGTTAGAACTTAAATGACCCCTGATTAATTAATG TAAACTGGTAATTTGTTTTTAAAGGCAATAAATTTGGTCTTCTTCATAAAATGGAAATTTAAA TATTTCTCTGATAGTCTTGAGGT/CJATCATTATGATAGTGCAGAAAGTGTG
WI-6824	112 A			CGTTTTGCTACACTTAATGGTTTTTTTTTAAAGGATTTTTTTCAGGTCTTGTGACGCAACATCAA ACAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCAAGAGTGTGCAAGAGTGTGCAAAATTTACAT GACACGGAGAAATGCGCTCTTCTCTTGAAGAGCTTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAAGTGGCAAGTAAAGGCAAAATCTTCTATCCCTTAGAGCTATTGTG
WI-6889	139 T	GAAAAATGAG ATGCAGTTAA T C A A T T C	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAAGAGCAACATGGAAGTGTCAAGAAACATCTGATAGGTACGGACAA AAGAGCTCTTCTCAATCAAGAGGAGTTACATATTAGTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCT/CJAGATAATTAAGGCCACAAAGTGAAGTGTGTTCTGGGCCCTATGTTGTAGATT CTCT
WI-6911	218 T			TCCCGAGCTCATATTTATTGGGCACAGAGTGGGCCTCAATCTGTGAACTTGTGAACTGAA AAGAGGTCTCTTAAACAGATATCATCTCCGAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAAGAACTTTGCTTCCCAAGAAATGTGTTTCTAATTTGGTTTCAAGCAGACTGGTTCC CACTTTTACCACCTT/CJATGACATTGGACAAATAGTACTCTTTTCTAC
WI-9413	112 G			GCCAGTCTCTAGTAAGTCTCTAGGACATGACACAGCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACITGGGTGGAGGATACCGCTGCTATTCCCGAGT/GCJAGATTTGGTGGGAAGGAG ACCATGACAGATGACAAACGGAGACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C			AAAAGCTTTAAAAAAAAGTGGTGCTATCTTTGAACACACTTTCAGCAAGATCAAGTAGCCAGCT ACAGCCT/CJTTGGTGCATCTTAACCCCTCTCTCTTT

WI-9617	37	G T	TGCTCTTTTATTACGTTTCACACACGCGTG(GT)TGGCAGCTCTACCAAGTGCCCGCAG CGCCACGCTTGGCGCGGAAGGTCTCTCTCTCTATGGACTGATGAAITTTGGATGGCCAG CTCCAGATGTTCCACGTGGGCGCACTCTGTGGCAGAGAGGCTGAGCCCTTGGCCACACTGGCACCA AAGAGGTTCACAGATGCAGCTTGCAGTGGTCCAAAGCGGGTGCTGTG
WI-9657	121	T G	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTGCTGAAGTATAGCTACCATCCACTAT CATGAAITTTTGTCTTATACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT(G)ATATTTCTT TGTTAAATAAATGTTTATAAATGTTTATGAAGCTCATACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAAATGCTTTTGATATAGATTGGAG
WI-13119b	114	G C	CCTGGGA	...	AAAAATTAAAC CAGGTGTGGTG T	CAGGCTTGCTGCTCTCCAGGCTAGAGTGAGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT(G)CACACCACACCTGGTTAA TTTTTTTAAITTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAACTAACTAAC CAGGCTTGCTGCTCTCCAGGCTAGAGTGAGTGAGTGACACAATCAAGACT(G)GACAGTAGCCCTCA ACCTCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAAITTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAACAACTAACTAA C
WI-13119a	51	C G	ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT(C)TCTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAATATAAATAGT TTCAATGTTATGTAGAGTCACATACATATGGCAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T	AGTTTTT	...	GGAAAAG	TGTTAACTTTTATTTGGTAGCTCTCAGTACAA(C)AAACAGCATCAGTAGTGACACTTTTGAT AAAAAGAAITTTTAGCTTAGTAGAAAGAAAGCCCAAGGTGCAAGATATAATGAATATGTACAT CTTTATGGAACCTGTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-12988	36	C A	CTCAGTACAA	...	CAAGGTGACAA CTACTGATGCT GTTT	TGCTATTATGACAGACACGTCAGACAAATATTCATTTTACAGATGGAATAGAACCCAGACATTA TTCACTACTTTAACCACTAATAGTGGAACCTGTGAGACTTTAG/ATCTGCAAGGGTTTAAATAT GCAATATCACATATATTTCCATTTTACACCATATTTAAGTTTCCATTTTCTTAATAGAAAAATGA TAAAAATGTTTCCCAATAT
WI-13020a	108	G A	CTTT	...	CAITTAATAAC CCCTTTCAGA	TGTATAAAATCCAACTTTGTCACCAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCAA/GTACAAAAAAGCAAGCTTTCTTCTATGGCCAGTTCTACAGAAGT AAGACTGTGCAAACTTTATGCTATAGTCAATGAGATTGCACACTAAGGCGAGGATGAGGCAAGCA AGTGTGTC
WI-12837	87	A G	AAAAGTCCA	...	GCCATAGGAA ATGCTGTTTTT	AGTGTGTC

L42611b	50 G C	GTCTCAGGCOCTTCTGGCTGCAGAGCCGCTCTCTCAGGTTCCTGCTGCTGCTCTCTGCTGCTCTAG TCTTCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGCTCTATACCT GCCCATCTGAGCACCCTTCTCACCATCAGATCAACCTTTGATTTACATCATATATGATTACCA CTGGAGCTTCACCTTTGTTAC
L42611	34 T C	GTCTCAGGCOCTTCTGGCTGCAGAGCCGCTCTCTCAGGTTCCTGCTGCTCTCTGCTGCTCTAG TCTTCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGCTCTATACCT GCCCATCTGAGCACCCTTCTCACCATCAGATCAACCTTTGATTTACATCATATATGATTACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTAATGTTCTTGAAATACCATTTCTGCTTTC AAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCTGTCAGTGAAATGCA CATGATGAGCCTGGAAACATGTTGT
WI-1172a	17 C A	TGAACGTGTGGTTAAAC/CATAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACAGTG GTGACCCACACCTCAAGCAATGATTATCCCTAGCAGCTCAGATTAATGTTCTTGAAATACCATTTCTGCT TTCAAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGGCCCTGCAAGTGAATGCA CATGATGAGCCTGGAAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTAATAA GACTCTTT	AGAGGCAGATTGGAAAGTGTGAAAGAAATGAAAGAA/CJAAGAAAAAAGAGTCTAAATATTTCAG AAATGTAAAGTGTGCCCTCAACTGTTCTTACCCACTTAATCTGCAATTTTGAAACACTAGATTGAAT TCCTTTGCAAAACCTTTGCATCATGGATACCCGAGTTAAACCGTTAATTAAGACATTAACATGCG CCTGGTG
WI-1231b	141 G A	TCCATGGTTGGTGTGCTACTGACTTTGTAGCCTTACTGCCACTATGCATTGGAACATTCOCATATTC CAACTAAGCAGGAGGTGTTCAACAATAACAACATAGGCTCTTTATCTCCTCTTTTCAATATTTCTT TCAC/GATTAATTCCTCACCTGACCCCTTCTCCTTCGTAGTGACATTTTAAAAATCCACTTTAC ACATTCGGACC
WI-1231a	126 T C A	GGCTCTTATT CTCCTTCTTTC ACATACATAT ICATTATACA	TCCATGGTTGGTGTGCTACTGACTTTGTAGCCTTACTGCCACTATGCATTGGAACATTCOCATATTC CAACTAAGCAGGAGGTGTTCAACAATAACAACATAGGCTCTTTATCTCCTCTTTTCAATATTTT CTTTCAGTTATTCCTCACCTGACCCCTGAAAGCCCTTCTCCTTCGTAGTGACATTTTAAAAATCCACTTTAC CATTCGGACC
WI-472	114 G C ACAGAAAAAG	GACCTTTCTTT TCCAGGCC	GAAAGGCAGGACTGTGTTTGGAGGCAAAAAAGTAAATCTTTTATCTTTATTTTAAATTTTAT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG/GC/GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATTTCTTAATGCAAGGCTGACAAATTTGGGCTTGATTT

WI-478	46 C T T G T T C	GCATGCTGTG TTACTCTATTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGTGTACTCTATTTGTTCTC/TAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAATCTCGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAGGCTACCATCAGTACCTTAGCACATTTAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C A A C T	ATCAGAGCAG AGTACCTTTCT	CCITCCAAOCT CTACACAATCT T	AGCCATCAGCAGAGTACCTTTTAACTT/CJATAAGATTGTGTAGAGGTTGGAAGGAGGACACGGA CTGTCTGTGTGTATATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112 T A	TCACCTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGCGGAACAGAGAGGTTTCTTGTGACTCTAACTGAGTAC/TI/CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	TCACCTTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAG/C/TJGAACAGAGAGGTTTCTTGTGACTCTCTAACTGAGTACTCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G C C T C A C C A	CTCCTTCACAA G C C T C A C C A	CTTCOCGGTAA GCCAAGT	AACAAAAACAGACACCCCTGGCTCTCTCACCGATCCACATGGTGCCAAACATCCACACTTCCT ACATCTCCCACTGGGCTGCTCTCCACAACTCACC/AJ/GJACTTGGCTTACCGGGAAGCATATAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT	TTATTTCTAATC CCACATGACAG C	ACTCACTGCTTGTGTTGTTGATTAAATCAACCTAGCCQ/GJGCTGTGATGTGGGATTAGAATAAAATA AACACAAAATGAAACACACAGATTGCTAACAAAGCAGATCTTTTTCAGGCACACGTAAAGAT AATAACTTCAA
WI-991	37 A T	TGCATTCAATTATGCACCAAATAAATCACTTCTGTACAT/TJ/CATTATTGTATTTCATTCACAAAAAT TATGAGTGAGGATGATTGTATCCCTATTTTACAGATGAGAACACACTGAGACTTTAGAAGAATATCT TTCCAAAGTCACAAAGTTAGTGACAGACGCGGATTCGAATCCATCACTTGAATCCAGAGAAAAAT GTTCTGCATCACTGTACACACTGACTCTTTTCTCTCCITTTGAAACAAAGGC
WI-1011	70 G C C A	CAGTATCTGA AGTTTTGTCT	AGGAACACCTA CAAAATGACTT CT	CTTCTGCACCTGTTGCAGTGGATGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTGTGTCTC A/GC/JAGAAGTCAATTTGTAGTGTCTCTGGGGTTTTTGTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGCTTGCAGACATTTACAGATGGCTGTTTGTCTGCAITCTGTGCACCTGAAG TTTCATGCAGAGGTCATGATTACAGAACTCAAGGAAGAGGCGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTGCTCATGAAATGGACAGACTGTTCACAGAGGAGGACAGCATGGAGAAAGA AAAAATCACTCTATCCCACTGCAGAACTGGCAATAGTTTGTG/TJTTACTAAAAACACAAATGT TTAATTTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5381	178 A T	CTATGATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCACAAAGATGAGAACAGGTCTCTA GAACCTCAG/GAJ/CTCGAAAGGAAGTTTCACTAGTCCATAGCCCTATCTCACTGACCCCAAGGTA AAAAATAAAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTTTGGCCACCCCTGTTTGT TAGGAA
WI-5791b	76 G A	

WI-5791a	44 C G	CTATGATTCCATCTAGCAAAAGCAAGACTATTGGATAGTTTTC/GACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAGTTCTATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTTCATTGTCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T	CACTCTGCTGTGTCCATGGTGCCACAGACTCTTCCAGAAAGGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTATGAGCCAC ACTTCTATTCTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGCTCAT	CACTCTGCTGTGTCCATGGTGCCACAGACTCTTCCAGAAAGGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTATGAGCCAC ACTTCTATTCTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5406a	42 A G ...	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAATATTT TCAAT	CACTCTGCTGTGTCCATGGTGCCACAGACTCTTCCAGAAAGGCCACTTCCACAGATGCAACAGGCC GCTTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTATTCTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5798	48 G C TG	TCTTCATGAAT TCATCTTTTCAG TTT	GGACTAAATTC TGATCCGATCT	CCATTCCTCTCTCCCTCTCCCTTATCTCCCTTGTTCCTTTTGG/C/ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACATATGTTAACAATGATGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TOCCAGAGAA AAATCCAAAGA GTTTAAG	GGACTAAATTC TGATCCGATCT	CCTGCTAATAATAATTAAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT/TT/ATTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TTACTTCCAGG CTCCAAGTAT	AGTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGAGACCTCCAGAGAAAAATCCAAAGAG/C/TCTTAAACCATATTTTGTGTTTA GAAACTCTGTGCCCACCACTCTGTGATGAGTGAC
WI-5481b	131 A G CTGCACTG	TTGCAATTTATG CCAAATTCAC	TTACTTCCAGG CTCCAAGTAT	AAGCCAAATTCACATTTGATGAATTTG/A/AAATTTACAGTATCTAAATGCAATGGGCATCTGTTTC AATCTCTGTTTTTCAAGAGGTAGTATATGTCGAAAAATCTATTTTGTTCATTTATGCTGCAGTCGAA ATACTTGGAGCCCTGGAAGTAAGACTTGGCTATTTTTCACAAATTA
WI-5481a	29 G A AATT	ATT	ATT	TCATGAGTCTTTCTTCAAGAGTGTGTTAAAGTCCCTTAAAGTCCCAATTC/CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA
WI-5492	38 T C	

WI-5967	165 C T	GAGTTAATGAATCTGTTCCCTCTAAACCTCCTGTTCCCTCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATGTAATGTAATTCGAAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATCTGTCTCCAAATCACCATTCCACTTTTATTCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C	GGGTAAGATCCAGAGCCACAGTGAACCTGCGCGGTATTGAAGTCTTTGGGCA/GC/GTCTGTAAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTTCCAACTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGGACACTGCTGACATTTGACATTTTCAGCAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAATAATTTGAATAATTAAGGCACCTTTTAATTAAGCAT CTACAAGGTACTTATTCJCACTGTTCTGGGTTTCACTCTTCACCTTTAGACTTCAGGAAT CAGAAAAATGCATGAAACAGGATTGTACATGCAGAGAAATAGGGGAGATAAAATTTGCTTTT CTC
WI-6450	45 T G TGCACA	CCAATGACTT ATTCTATATCT	CT	ATAGGACAGTTTTCTCCAAATGACTTATCTATATCTGTCAAT/GAGAAGTACCACACATTTCA AACAAAGCCAGGCTATGCCAGGTGGGATTTTTCACGGTGGTAATATGCATGTAAAGACTA TTTTACTGGCCTTCTTTATGCAATAAACCAAGGTATTTGGTCTATTCAACAAACATTTGTCAATACAG CAGTTGTCATGTCCTCTGGTACTAGAAATAGTCTTTATAGAAATATGTGGTTTGAATAAAGCCACA AATTATTTCTATAAACCAACAC/C/TAAGGAACGAGGCTCAAAAGTGAACAAAACGGCCTTAGTTTC TAAGTGGAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-6461	88 C T	GAACTATCCTTTAGTGGTGCACATTTCTATTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTAGTGAACACTAGTTATCATAAAGACATGCAAAACCTTTTCACAGCTTTGT CCTGGG/AJAATATCTACAAAATTAATTAATAATTTGGCATGGGACTTTCTGATTTAGCCTGACAGG ATTGTCCTTT
WI-7466c	141 G A TTTGTCTGG	TTTCACAGTC	AGTGGCATGCC AATTTATAATT	GAACTATCCTTTAGTGGTGCACATTTCTATTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT/CJATTTCAGTGAACACTAGTTATCATAAAGACATGCAAAACCTTTTCACAGCTTT TGTCCTGGGAATATCTCACAATAATTAATAATTTGGCATGGGACTTTCTGATTTAGCCTGACAGGA TTGTCTCTTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA	ACTGAA	TGCTTTTAAAAATACAAATGACCACCACTGACACCATAGTCTGTCTCCATTTGCCACGCTTCTCCTC AGTAGAAATAGACAGGAGGACTTTGCTGGCTGTATCTGCTTTCTGCTTTGAGAGGACACTTTGGCCCT CATAGGCAITCCATAGATATTTGTTGAATGAATGTGCTTTTTCATATTTGATTTCTACATTTGATACA TTCTCAGGAGGACATTTGGCCTAT
WI-9814	104 C A	CCTCTAACAAAGAAACCTTGACTCTCCTCAACTCAAAATACCCTTCTCTATAATTTTGAAGTAACCA AAATAITTCCTTCAATAAATAATCTTTTAAITAGAGAAGCAACAGTGTAGAGGTAGTACATTCA CCAC
WI-9720b	55 A/G	

WI-9720a	47 A G	CTCTAACAGAAACTTGACTCCCTCAACTCAAAATACCCTTCTTGAJATAATTAAGTAACCA AAATAATCCTTCAAAATAAATTAATCTTTTAATAGAGAAGCAAGTGTAGAGGTAGTACATTCA QCAC
WI-9825	123 A T	CACGCTAAGGCAGATGGGCTTATGAGATACTTTGCATTGCTGTCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTGTCATGTGCAGATGAAGGCTCAGGGTGTATAGAGGATTAG TAAAGATCTCTTTCTAAAGACAGAGAGATTATTAACAAGAAGAACTCACCAGGGTTTGTGCAATT TAAGAATTGCCAGTCTTTTGCTGCTGCATCATCTTGAACATTAATOCACATG
WI-9748	74 C G	CCACTTCAGTAAATCAATTTGTAGCACATTTCTTAAAGATTTCTAAATTTTATATGTTTACCCTTT GTCTATTCGTCAGACCAAGTACATGTTTTCACACAGCATCTTTCTTCTCGGAATCTTTCAGAAT TACAGTTATGATGCTCTTTTATATCCCA
WI-9943	91 T C	TGAGGCTATGATTGCAGATTGTAGTGACTAATACTTATTAAGCAATTTCAATGTTGGGCACCTGT CGTTGGTTTATATCCATCTTCTTCTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTTGCTCCTTATTTGTACCTTTTAAATTTGCATTTACACCTCTCTTTTGTCTATTAGGSA
WI-9891	39 T C	AGGGGCTTCACAGATCCGTCAGCTCAACACTGCTCTCTTGTGAGTGAGCTGTGAACCCCAAGAC GGCTGGTCACTGATGTCATCTCTCTCTTCCGGACAACATCTTTAAAGAAAAAAGAGTGT CTTTGAATGATCCATTTTATCCCAATAATCTTTGTTTAAATCTCTTATAGGCCAATCCAAAT GTGCTGAATAATCTGCCAAGCATGCTCTACACAAAAGGATTTGCAAA
WI-9897b	84 C T	CTCAGAAATTCAGATCTTCCCAATGTCTATGCTTCTCAACATCTTATTTCTCTCAAC ATTTATCTAGCCTGTATCAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
WI-9897a	83 A T	CTCAGAAATTCAGATCTTCCCAATGTCTATGCTTCTCAACATCTTATTTCTCTCAAC ATTTATCTAGCCTGTATCAAGTCAATCCAGTGAGGCTGTTTATTCATCTATGTGAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
WI-9935b	115 C A	AGATAACCCCTGGAAACTAGAGAATAATTAACGTGTGACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTCTTGGACTGGCAGGGGAGTTGAGACATCAAGCAAGAAAGGCC TGATATTAGAGGGCACTTGCATTAA
WI-9935a	42 C T	AGATAACCCCTGGAAACTAGAGAATAATTAACGTGTGCACTTGCATCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGGTCTTGGACTGGCAGGGGAGTTGAGACATCAAGCAAGAAAGGCC TGATATTAGAGGGCACTTGCATTAA
WI-9983	146 C T	CCGTGTAGGTGGCAGAGTCCATGCTTGGCCACAATGTAGGCTGCCCTCCCATTTCTTGTCTGA TTCCCAACCCCAAGGTTCTACCCCAATCTGATCAAAATGCTGATGCTGCTGGTGGTCAAGGTAA AGCAATTATGATCACTGAGACACAAAGAGAGGTTAAAGTTGCTGCTCTCAAGAGAGAGACATAA AAACAATGATCTGGAATAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T A T C T	T G A T G T A A T G C T A T G T A G C A A	T T G A T T A C T G T G C T T A G G G G A	A T A T C A G T G G G T T G A G T A T A C A G C A A T C T A T T T T G T T A T T A T T A T G T G T G C T A T A A A T C A A T C A A T G G T T C T A A C A T T C A A A T A A G A T C T T T T T G C T T C T G C T C A G A T G C T T T C A A T G A T G A T G A T G C T A T G T A G C A A A T C T A T A T T C C C C T A A G C A C A G T A A T C A A G G C C T T C T A C C C C A
WI-10020b	122	T A T T T	G C G A G A A A A G A A A T C A T G A C	G A C T G T T A A T T T A T T T A A T C A T T A G T C T G G	T T A C T T C A T T G C A C T T G A C T G T A T T A A A T A A A T T A T G T T A A C T G G C T C T G A A A G A A T T T A G G C A T G C A T A G A A A T A G C A G T G T T T T A T T A T G C G A G A A A A G A A A T C A T G A C T T T T T A A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G C C T A G G G T T C C G G A A G T G G C C T A A A G C A C B T A G T A G C C C T C C T T A G A
WI-10020a	39	T C A T A A A T T	T G C A T C T T G A C T C G T A T T A A	A A A T C T T T T C A G A G C C A G T T A A C	T T A C T T C A T T G C A C T T G A C T G T A T T A A A T A A A T T A T C T T A A C T G G C T C T G A A A G A A T T T A G G C A T G C A T A G A A A T A G C A G T G T T T T A T T G G G A G A A A A G A A A T C A T G A C T T T T T A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G C T C T A G G G T T C C G G A A G T G G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10064b	170	C T T T A G A T A T A T T G T G A T T G T T T A C A T G	C C T T T A G A T A T A T T G T G A T T G T T T A C A T G	A C C T T T C T G A A G C C A G A T T T C	T C T G A G T C T T T C T G A C A C A C T T G C C A T G G T C A A G G G T A G C A G G A T C A G G A A G G C A T T A T A A A A T A T A A T T T G C A G A C A T C T C T C T C T A T G C A C C A G A T A T T G T G G T G A C A C T C T G T T T A A T C C A G T A T C C C T A C T C C T T A G A T A T A T T G T G A T T G T T T A C A T G C T T A C A T G C T T C A G A A A G G T T A G G T G T T T
WI-10064a	54	C A C A G G A A G G	G T A G C A G G A T	C A A A T T A T A T T T A T T A T	T C T G A G T C T T T C T G A C A C A C T T G C C A T G G T C A A G G G T A G C A G G A T C A G G G A A G G C A A T T A T A A T A A A T A A A T T T G C A G A C A T C T C T C T A T G C A C C A G A T A T T G T G G T G A C A C T C T G T T T A A T C C A G T A T C C C T A C T C T T T A G A T A T A T T G T G A T T G T T T A C A T G C G A A A T C T G G C T T C A G A A A G G T T A G G T G T T T
WI-10289	29	T C A A A C T C T T	T C T C T G T G C C C A A A C T C T T	A T T C T T G T G T A T T G A A T G G A A T T A A	C C A G G G A T T C C T G T C C C C A A A C T C T A T T C T T A A T T C C A T T C A A T A C A C A A G A A T T T A T A G A A T A T G C A C C A C A T G C C A C A A A G A C A C C C T A T A T T A G T
WI-1319	40	A T A T T C T T T	T G G C A C T T A G A A C A T A G T T T A T T C T T T	G C C A C A C A C C C C T A T G T C T A T G T	A A G A A A A T C C T T G T G G C A C T T A G A A C A T A G T T T A T T C T T T A T A C C A T A G G G G T G T G G C T T A T C T T T A C C T G G C A T G C T T T A G G T C C T G T T A A T T T G G T A T C T T T T G C C A A A A G A G T C T G T T C T G A C A G T C T T A T G A T C T C T A T T T A A C A T T A A C A C T G G T C A G A T G T T T A A A C T G T T G A A C C T G C A C C T G C A G C A G C A A C G T G T A C A A C T A G T G A G G T G T A A A T C A G A A G A C A T C T A T A T T A T T C A C C A G T C A C C A C C C T G G A C T A T A G T C T G T T G A T T T T A C C T C T A T C T T A T C T A A A C T T T T G G A T A C A T T C C A A A G C A T C A T G G T C A C T T C C A G T A T A A A G G A T T T A A A A G C C C A G C C A G T G A G T T G T G C A C A A T T T T G G A C A C A T T C T G T G A C C C C A A C T T A A A C A C A C T T C T C C C A C A C T T A G
WI-10316	104	T C C T C T T	C T A C C T C T A T T C T C T C T T	T A T C C A A A A A G T T T	A A G T T A A C A C T T C A G T T A C C A G G T G A T T G A G C A G A
WI-2572	61	C T T

WI-10368	31	C T	TGAAGCAACC AGGTCTTGTT	CAAGATATTAT ATTATTCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCAGGTCTGTCTCTACCCCTCTAGAGATAAATAATATCTT GAGATAGGGAGGAGGACGCTGAGGACAGTCTGGGTTTGTCTACCCCACTGGAGGACGAATATCC TTCAAAGCTTTTCCAGTGAAGTCTGCTGCTAACTATATGACCTGATGGATTGCTTTCAGGG T
WI-10391	32	A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CTCTCCGTTCTCTGTCTCAGGTATGACTCCCAAGTCAACTCTCTGACTCCTAACCTCCCATCTCGGTG TCTGCTTCCAGGGGACGCTGCTGACACAGCCTTTTGTCTGCTGTGACAAACAGAACATTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146	A C	GTTAACCAGA GTCTTCTAATA	TGCGGCTTCCA GTAGCT	AGGATGAATTTATATGTTATGCCCTGACTAGCGGGTGCCTCAATAAATAATATTTTTCATATT TTCCAATTATTAATACTAGAAATTTTCCACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATGCAAAACJAGCTACTGGAAGCGGCAAGAAATTTAACCTT
WI-10567b	82	A C	AGGATGAATTTATATGTTATGCCCTGACTAGCGGGTGCCTCAATAAATAATATTTTTCATATT TTCCAATTATTAATACTAGAAATTTTCCACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCTT
WI-10567a	60	T C	GGGTGCTCAAT AAATATTATT	AAATTTCTGTT GGTGAATAATTC TAG	AGGATGAATTTATATGTTATGCCCTGACTAGCGGGTGCCTCAATAAATAATATTTTTCATATT ATTTCCAATTATTAATACTAGAAATTTTCCACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCTT
WI-11153b	84	C G	CAAACTTCAA ATTGCTTTAAG	AAATCCAACA GTCAAGGCTTT C	CGTTGGGAATTTCTATCTCACCTAAATTTATG/CAGTGAATTAATAATATACATTTTAACAACTTC TTGCTTTAAGTACTTTAC/GAGAGACCTTGACTGTGGATTTTGAGTTTTCCTTTTCTTTTCTTAATA AAACATGTCATATTTAAGTTGTGAGCAAGATGACTTATATGTTAATTTATCTGATATCAGCATCCCTT TATGTAAT
WI-11153a	33	A A	GGGAATTTTC TATCTCACCTA	GCAATTTGAAG TTTGTAAAT GTAT	CGTTGGGAATTTCTATCTCACCTAAATTTATG/CAGTGAATTAATAATATACATTTTAACAACTTC AAATTTGCTTTAAGTACTTTACGAGACCTTGACTGTGGATTTTGAGTTTTCCTTTTCTTTTCTTAATA AAACATGTCATATTTAAGTTGTGAGCAAGATGACTTATATGTTAATTTATCTGATATCAGCATCCCTT TATGTAAT
WI-2816	125	T C	CACAATGTA ACAAGAATTG	CCATGGCTGTA GTCCAGT ATCC	GTGTGAATTCAGTATCATTTTCCCTCAACACCGCTTAATCAACATCATTCTTTCTCTGTA GAGCTCAACTCAGTCTGAATGAATTTGCTGCACAAATGTACAAAGAAATGATCCTAT/CJACTGGG ACTACAGCCATGGAGAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58	C T	CAAGTGAATT ATGACCAAAA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAGGAACACACACAAAAAGTTTACCAGAGTGAATATGACCAAAATGAG/C/TAAT TTGTTAAAAAAAACCTCAAAATGAAGAGAGCAAAATATAGTTCAAAAGATTCAGGTTCAATATTGT ACCTACAAAAAGGGATAGTCAATGGTTTGGCAGACTTTTCTTTCTTTTCTTTTGT/GJCTTTA GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCCATATTTTAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCAGAGTTCTGCTCTTCCCAATCCAGAGGAGTACTATTCACCCCATGGGGTCAAT AGAGAGGATTTAAACAGGGTGTGCTGCTCAATGGGAATATTTGAAAAAC
WI-10656	59	T G	

WI-11169b	154 T G	TTAACCAAGA GTTTTTCATTC	CTAACTTAAAA ATCCTCAITCA	CTGACTTAGAGGCTGTAGTGACCTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAATTTAAGCCTAAAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTTTTT TTTAAAAAAGAGCAGACAT/GJTTCATCATGTGTTCTGATAAATTTTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95 A G	AATAAGTGAA AGTAACTGAC	AACTCTTGGT TAAAAAGCAC	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAATTTAAGCCTAAGAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAAATTTTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G	CAAGTGTGGACCTTGATAGGTC/GJACCGGCTGAAGGTGGACAGTTGTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTTCCTTTGGGTTTACCCTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATCCAAATAGCCATGGGTTTGGACAAATAC AAGGTTAGTGTCTCTAACTTTAATGGGCATA
WI-10686	133 C T	TGCCCCGTGTC AAGG	CAATCTCTAAA TTCATGTGTAG	AAATAACCTGTGGCACAAGGCAATACTGAGCCCCATACAGAGTGTTTTATGTTAATATTATGAAA AAAGTCAAGAGAACAGATGATAGTTCTCTAGAAATCTGAAATCTGATGCCCTGTCCAAAGG C/TJTGTTGCTACACATGAATTTAGAGATTGAATGAATAATGGCAAAATTCAGAAAAAGGG
WI-11175	77 T A A	AAATGATTCTT TCTGCTCAAG	CTGTTCTCACA TCTTTTGGAA	GGTAGGATGATTCTAGAATGCCACTTTACGCCACTGAATATATGCCCTCCCAATGATCTTCTTG CTCAAAAGAGT/AJTTTTTTTAAAGTTATCTACTTATTATTTATCTGCTTTTTTCAAAAAGAAATGTGAGA ACAGTACAAATGTGTTTCAGTATAGCAAAATTAATTAATTAAGTAAAGAAAAAGCAAAATTT TGCGC
WI-10694	144 A G	TGCAAAATGCTT TATGATGATTTTC	GGCATTITGTA AAGGAGGAAA	TAGAGAGTCTTCAGTTTCAGGGTTGGAGGGTGGTGAAGTTCAGTTCTCTAGAACACTGGC TATGTACAGAAAGATAAAGTCTGAGAGAACTCAGTTCTAAAGTGTTCAGTCTTTCGCAATGCTTTA TGAGTTTTTQ/GJTTCCTCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT
WI-2716	23 T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTCTC TTC	T GTGAATTCATCCAGAAAAAGCTT/GJAAATGACAACAAGAGAGAAAAAGAGAAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCAGTGCATGGAGCAGTG
WI-10719	115 T C	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCACTCTGTCTAATAGTGTTTTAGAACACACACCTCAGTACACAAAGTTTCTCTGTATGT GCCACCAATAAAGAGTACTGGAGGATGACTCTCAAGGCCATCTAGTCTGGCTGGCAGTGCTT TTCAGCCTGTGCCCATACTAA
WI-10721	40 A G C T T G C C A	TGGCTCTGCTA GCTTGCCA	GAACTCCAC ATAAATAAT	CAACCAATTCAGATTAAATTTTGGCTCTGCTACTTGCCCAAGATGAGATTATTATGTGGGAGTT TCTGAAGATCCCATGGTAATAGTATCTCTTCCCTGCTAGGTTTGAAGAGATTGAA

WI-11204b	88 T C ...	GTAAAAGGG TGAAAAGAAA	... TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTTTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA	... TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTTTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTTCAC	GTAAAAGGG TGAAAAGAAA	... TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTTTCAGAAG GCAACATC
WI-11206	127 A T ACTC	GTAAAAGGG TGAAAAGAAA	... TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTTTCAGAAG GCAACATC
WI-11215	68 C T ...	GTAAAAGGG TGAAAAGAAA	... TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTTTCAGAAG GCAACATC
WI-11219b	89 G A AGAGAAA	GTAAAAGGG TGAAAAGAAA	... TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTTTCAGAAG GCAACATC
WI-11219a	18 G A ...	GTAAAAGGG TGAAAAGAAA	... TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTTTCAGAAG GCAACATC
WI-11222b	136 G A GCCTGG	GTAAAAGGG TGAAAAGAAA	... TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATGATTAAATATTGGCTGACTTTGAGGAGGAGACAGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAAAGTCTGAGGAAAAATTTTCAGAAG GCAACATC

WI-11222a	25 C T A	GCCACAGTGG AATCAITTTAC	TTTTAGCAITTT GCTGATTTCCG	AGCCACAGTGGAAATCATTTACACTATCTGAAATCAGCAAAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTTTTTCATAGACCCCGTTGAACCTATTTAAACATTTACCAGCATACCACTGCGG CTGGGTCCAACTTGGCTACAGGAGAACTGACACAGACTTCTGTAATTTGCTTTACAGGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATATGCCATAATTAATTCATTACACTCTCTACATCATATTTTCTTAGCAAAATACA TCTAGACACTGGCACTCAGTAGGGATATCTCTGACCAATAATCATTTGTTATTCATTAGACATTTGCA GGAAACCACCATATGGATGATAATGTGTGTTTAAATGAAGGCAAGCAATTA TTGCATGCAITTTATACGAAAGGAATTAATAATATCTCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAGTATAGTAAACAAATAGTAAATTTGTCAGTGGTTGG TAGTACAGGAATCAAAATTTGGACTATGAACAATCTGCTAAGGATATTCACACAAATTTAT TTCATGA
WI-11226	165 A C	GOAAGGGAGG AACATTTTACA	CTGGTGACATC AGAGATGGAC TTGAGGGACCC TGGA	CAGTGGCTGGTACTGACAAAAACGTAACTCGTGGCAGGTGGCAAGGGTGTGATCTGGAG TCCATCTCTGATGTACACAGAGGGCCAGGAAGGTTGATCTGGAG TGGGACACACTGCTCTAGACCTCTCTCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGAGCCAGAGGCATCAGGGCCCTTAGTCTCTCTGGGACAGTGAAGGGCCACCAAC ACAGAAAAATGCTAGTCTTGTAGCAAGAGAGGAAAGCATCTTTCATGGGACAGGAATTTCTCATTT CTGTGTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTCGATCCAGCAACATT TCGGTAACCTACCTCTAGAAATCATGCAAAAGAAATGATGA
WI-10810	58 C T GCAGGAAT	CATCTTCATGG GCAGGAAT	AAACACAGAA ATG	GGACCAACAGAAATTAATCTGGCAATCTGAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAAGGAATACAGTTAGGGAACATGTGGATGAATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATTTGGATACATTTAGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATCTAA
WI-10828	23 T C			TATGCCITCCCACAGCAGCCATCCACGCTGCTTTAGCAAAAAAATAGAAATACATCATCTGAATG GGCATTAAATCTGACGGCTCTCGCTTCTAAGTCCCTGCAGTTAGGTCTGCAGACACTGTGTGA TACCATATAATCTGATTTCTGAGCAGGAGGGAGGAGATGAGAGAGGGCTGCTCGGTGAAATAC TAGTTCCG
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	A	GATTTGAGTATTAATAAAATTTGCCAAAGACCATTAACAAGATTTAATAGTTAAAGCCAAACATATA AAGAAATTAAGTGTCAAAGGTGTAAATCTCTAATACCAATTTTATAGGGCCACCATTTAACTT CTGAAGAAAGGTGACATATGCAACTAAATTTCTAAAGTCCAGT
WI-10834	96 C T GTGTTAAT	AGAATTAAGT GTTCAAAGT	TGGCCCTATAA AATTGGTATTA AG	GGATGATGTTCTGTGGTCCCTTTATCTAAGGCTCTTGCATCCCAAAATGTGTAAATTTTATTTCT TGGTATTTCTGCTTAACCATAGTCACTGTCAAGTGTCTCCACCT
WI-2287	24 T C			

WI-2296	81 A G G A	TGTTACTTTGA TTCITTTGCTCT	GCAATCACAC AGTAACCTGG	TGGAGGGTTAGAAATGCAGGTGGCATCTAGAAAGTCTCAGGCTTTAGAAATAGTTGTTACTTTGA TTCITTTGCTCTGACAGCCAGTTAGCTGTGTGATTGCAAGAGGTACATTTGTTGTTG
WI-2300	77 G T C C A G T C A T A C	GGCACAAG CCAGTCATAC	GGTTGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCTTTATTTGAGCGGGCAGGTGTAGGCACAGAAGC CAGTCATACGTTTGCITTTAAATTTGACCAACCATTAATAGAAATAGCATTC
WI-2371	55 G T C C C A G C T C T	GTCTTGTTCTT CCACGCTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAAGTCTGTGCTGTATTAATCCAATCCTTGCCTCCAGCTTTACATGATGT GTCAATCTTTGACATTCCTTGTCTTGCAGCTGTATTAATCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCGGTGTCTGTG
WI-2395	122 A C T A C T A T C C A A	GAACATATT GTAGAAAAAT	TCACCTTTCTA TTTATCTGAA	GGGGGCACAAATTTAGCTACAGTGCATATTAAGAGTAACATAGAAATATCATATAACTTTGGTTTAC TGAAATCTGAAACATTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCCAAACATCTGAAATTC AGAATAATAGAAAGGTGAATCATCTTATATCAATTAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G A		...	CACCAGCCACCACCCCTACAACTCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGATGGAGTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGAG/AGCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G A		...	CACCAGCCACCACCCCTACAACTCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGATGGAGTCAACCCCTTCTCTCTGCAAGAGGCAATCGAC/AGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G A		...	CACCAGCCACCACCCCTACAACTCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCCAATCACAACCTTTCTAAATATAGACACCAAAAAATTCCTCAATG/AGCTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G A	GCAACCTACT GACAAATTTAA TTTATGTT	AACAACCTCTGC TATTTGCTCA C	CAGTAGGAACGGGTTCTCTCTTAGACCTCCAGAAAAATTAATGCAACCTACTGACAAATTAATTTA GTTG/AGTAGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T C G A A A A A	TGTTTAGGAA ATAATGACAA	TGGTTACAACT GTACCAAAACAT G	CTGTAACCTACACACATCTCTCTGTAACTCTAGGTTACTTGTATACAAAAACACAAATGTAAATGCT ACATAAAATTTGTCATCTACTATATTTGTTAGGAAATATGACAAAGAAAAAGGCC/CTGTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCCCAATATTTTCAATCCACAGTTGGTTTATCCACAG AAACCACGAATG
WI-2886	46 C A G G A G A A G A	CAGAGTCTGG	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAGGCTGCAGCCCTGCAGAGTCTGGGGGAGGAAG/CAACAGAGATAAGCATG GCAAGACCCAGCTGAAAGTATCCAGGGTGTGTATGTGCAATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAGGTGTACAGAAAGACAGAGGAGCGTT

WI-2906b	77 T A ...	GACACCTTCAT	AGAGCAITCCA	...	CCTGAACACCTGGAGCACTTCCTCCCTGGACACCTTCATCTGCTGGAACCTTTGCTGGAATGCTCTGCTGCTTAAGAGCTTTGCTGGCTTACTTTTCTTTCTTTAGGTTTACGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50 A C TCTGCTGG	...	GGCAAAAGT	...	CCTGAACACCTGGAGCACTTCCTCCCTGGACACCTTCATCTGCTGGACACTTTGCTGGAATGCTCTTTCCCTGAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGGTTTACGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175 C T	TACTCCTCATTCCTCATGTCCTAGACGCTACTCAGATTTCCATGCCCTGAAACATTTATTCCTAAATAGATTTCCACCCCGAGCACTATTACACAGAACAGCATGGAGCTTTGGAGTCTGGCTCTTAGAGAACTTACTTAAGGACAGTGGTTTCCATCTGCTTCCA/CCTAGAGATCTAGGGTGTCTTTGGAACCGACCTGG
WI-1851	136 G A GTGTTAAGTA	GCATTGAATT	CACTAGCAATG	...	AATACCCACGCTCTACACCAATCAGACTGATCATCAATCAGGTTTAACTATTAACTCTGGGGAGGACACAAACATTTAGACCATAGCAATTGAATTAACCTAGATGTGTTAAGTAATTTAATCAATGGTACA/GA/CACAACTCAGTTTAACATTTGCTAGTGAATTCATGTGGATACCATTCTTTACATCATGTGA
WI-3000	62 G A AGAGACCC	CCCAAAACAC	TTAAACTGAAG	TTG	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTCAGACCCCAACACAGAGACCCCGA/ITGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177 G A TAGTC	TTTCTCCCTT	AAAGTCGAATT	...	ATGGATCTGCTCAATTATAGTCCAGATAACAGCCCTCTCCCGGCCACCCCGGATTTATTTACTTAAGGGTTTAGCAAAATTCACCTGACGTAAGAGATTAAGTTTCAACATGACCCCTCATAAAGTGATTTTCTCTCTTCTGTTTCTTCTCCCTTCTTAAGAGATAGTC/GA/CACAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A TAGATTC	AAATCAACC	TGTGATAGTTT	...	ACAAACACAGCAAAATTCACCCACAGATCTATTAGATTCT/A/CACCCATCTCAAAACTATCACATCAAGAAAGCAAGGAGACATATTACTGTGAGGAAGCCAAATTCAA
WI-3208	140 G A AGATAAAGA	GTGGAGTGGGC	TCACCTCAAAC	...	CAAGCACACATTCAGGCGAGGTGGGCAAGGTGGGCAACTTGGCCAGCAGAGAGGAGGAAGAAAGTTCAGACCGTTGGTAGGATAGTGGATCCAAACCCCTTTAGGGCAGGTTGGAGTGGGCAGATAAAG/GA/CACCAAGCCCTAGTTTGTAGTGACACTGTGGGGATTCAAG
WI-1775	47 C T TTTTCTCTG	CCTGCATGGTC	ATGACAATGAT	...	ACTCCACAACAAGTTTGTGAGCCCAACCCCTGCA'TGGTCTTCTCTG/C/TTTACATCATTTGTCATAATCTCAACTGACATCATGCTCTGCCCCCA
WI-3402	55 G A /ACAT	AGCATATTCA	GAGGACTTAAA	...	CTGCCCTTTACATCCAAAGCAGATTACTCGAGCATATTCATTGATTTCCCTTACATG/A/CAAATGCTCTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCAACAAATAGATTTCTCTTAGGA

WI-3416	33 C T	CCAAGTTGTA GCAATCAGAA	ACGAGCACAA CTACCTCTAAG AG	TC TGGTTCCTCCAAAGTTGAGCATTGAGAGTCTGCTCTTAGAGGTAGTTGTGCTCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACCTCTCCCAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGTACCTCTGACGCAACAATAATTAATCCCATTTGCTTAAAGACCCAGG TCCTATTCTTACAAACACAGAAATTTAACAAATTTGAAATTCAGCTACTCTCTTAGGCCCATCAGAG AATTC/TAAGTCAATGCGGAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACAGGGACACAATCCACTTCCAGAGCCATCATCTGTAAAGAC CATGCTAGGTAGTATCTGATGAAGTTTGAACAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTTATGAGGTGGTGA/ATGGAGAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCACC
WI-3453	70 C T	TCTTAGGCC ATCAGAGAA	TCAATTTTCC CATGACTTC	ATTC/TAAGTCAATGCGGAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACAGGGACACAATCCACTTCCAGAGCCATCATCTGTAAAGAC CATGCTAGGTAGTATCTGATGAAGTTTGAACAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTTATGAGGTGGTGA/ATGGAGAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCACC
WI-3474b	109 G A	AGTCAGTTTCC CTAAATTTAGC	CAACCATCAAT TTTCTCCA	CATGCTAGGTAGTATCTGATGAAGTTTGAACAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTTATGAGGTGGTGTGGAGAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCACC
WI-3474a	90 A G	CCTGGGTTTCT GGATGTCT	GGGTGAACCTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCCATAAGAAATGGTGGAAATTAACGGGAGAGACCTGGG TTTCTGGATGTCTCT/TTGAGGACAGGGTCAACCCAC
WI-3502	79 C T	GGTTTCTAAC TGGATATAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGAACCTTCCCTGCTTTCAGAGTCTGATTATCCATGCCCTG ATAGTCTGTGAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGGATA TAAACATCTG/ATGGAGGGCTGCACCTGGATGAGGTACAAA
WI-3500b	146 G C	CCATCT	CCATGCCCCTG	TCACGGCAAGTTCTGCAGCAGTGTCTTGAACCTTCCCTGCTTTCAGAGTCTGATTATCCATGCCCTG ATAGTCTGTGAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGG ATATAACATCTGATGGAGGGCTGCACCTGGATGAGGTACAAA
WI-3600a	78 T G	ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTACAAAGGTATCCACTCACAATAGGCAATTTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAAACCTTCTACTTACTGCTGTTATGATGCACCTG/TCCTTTTGG ATAGATGGTTGATAGGAGATGGGTGTTAAAGACACAATTTACCTTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTAACTCACTGAATGAGTTCCAAAGCCTTTATGTCTTAC
WI-3678	125 G T	---	---	AAAGCGATTTGAGATACCACTCCATCCATGAAAGTAAACACACACACAACAATAATGACATAAAA TAC/TAACAACTACTATAGTTTATGAAATGACTTCCAAAATCAGAGAAAGTCACTTAAACAGG ATTCTCAATTCATCCAGATACTCTGTCATCTTAACTTTGACTGCACAG
WI-3687	67 A C	---	---	TCTAAATGTGAACCAAGAAATCCTGACACGACCTAACTGCCAGTCCCTCAGTTATGTATCAAAATGA AAAAC/TAACACCGGTTCATGAAATAACAAATGATTTGGTGGAGCCATGTCCCCCTTATTTAATGAAAA GATCTTGGGCAATTAACCTC
WI-3735	72 T C	AAAC	GGCTCACCAT CATTTT	

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WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCTGCGATATACCTTCCAAATGACTAGTATGAATAAGCACGTTAAATTTACCTATTATATTT ATTCATCATGATTTGCTGCCCTTCTTCCAAATTTACTACAAATTTGTTGTACATGAGGCACATG ATCCCATTAACCCCAATAG
WI-4199	51 A C	CTCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTTG	GCCATGAGCACAGAGGCTGAACCCACTCCCAAGTTAGTCAATATAAAAAAAGC]CACACATATTG TTATACCTAATCAACATATAATGTTATAGATTAAACAGTCCACAGCAACAA TTCTGCTGTCACTGTGCTGCCCTGTTCTGCTGCTGCTGCTGCTTCAATGTTCACTGCTTGTAT CTGTGCCACTAAGGTATCAGGTTATATGGGCACAGGATGAGGGCTTTGTAGAACAGAGTTTCTT GGAAATTGCAACATTTGGGCAT
WI-5163	24 C T	CTGTCACTGGT CTGCTGT	AGGAACAGAC C	TAAGTGCAATTAACGTACAAAGTCCACAAATACCTCTCCACCAAGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTGTGAACAGGGGTGGGAAGGATCCTGTAAAGG]A/GTTAAATATTGTTTT CCATAATTTGAAGATGTG
WI-4250b	117 A G	TCAATATGAG TCTTGTAAG	---	TAAGTGCAATTAACGTACAAAGTCCACAAATACCTCTCCACCAAGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTGTGAACAGG]GTTGGGAAGGATCCTGTAAAGGATAATAATTTGTTTT CCATAATTTGAAGATGTG
WI-4250a	94 G T	AGG	CTTTACAGGA TCTTCCAC	TAAGTGCAATTAACGTACAAAGTCCACAAATACCTCTCCACCAAGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTGTGAACAGG]GTTGGGAAGGATCCTGTAAAGGATAATAATTTGTTTT CCATAATTTGAAGATGTG
WI-4255	68 G C	TGCTCCCCCAT CACCT	GGCTACTTCA AGTTGTGTAAG G	TAAATGCTGGGAGATAATAGGAAGGTCCCATCCCTCTGATACCTTGGTTGCTCCCCCATCACCT G/C]CCTTACACAACTTGAAGTAGGCCCATCCAAACACTGTGTACAGAGAGTAATCTGTGAC ACAGCCTCTTCAAATGGCACAAATCAAAAGCAGTAAAGCAGAGGCAAAATCTGGTCTCAG CATTGGAAGTCTTCTGAAGGATAAGGAGTGAATGACTGCTAGAGAGAAATGATTGGCTT AGTTCACTGCTAGATGAGTAGACCATGTTGCTTTTAAATGATGATGGCAGGACCCGGAATGG GATG]TTACTATAGATAATCTTTTTTAAATGACTCTTCTGGTCTCTTCAAGATATCACCGCCAC CCAGACACTGCCATATCT
WI-4325b	71 C T	---	---	AGTTCACTGCTAGATGAGTAGACCATGTTGCTTTTAAATGATGATGGCAGGAGC]T]GGA TGGGATGCTACTATAGATAATCTTTTAAATGACTCTTCTGGTCTCTTCAAGATATCACCGCCAC CCAGACACTGCCATATCT
WI-4325a	58 C T	---	---	TGGGCAAGAGTCGGGTATGGCAAGTCAGGTTGGTTAACTGGATGCCACTTCTGCTGTCACCTTCT CTAGACTCTTGACCCCTGCAGGAGGATCCCTGGCTCTGATTTTATCATCTCCACCTCCAGGCCAG GGCCCTGTATCTGTTACGGCC]AG]GAATCGTCACGGCTCACAACATGTGGGAGGTAGGAATGACGA G
WI-4347	158 A G	---	---	CCAGTCTAGGCTCAAGCACTTCAATTTCTGGGCAAGTCTGCTGTTGTTGCTAGGGTCAGAGGCGG ACCTGAGGGGACACACAAGCCAGTGGGACACCGGGGTACTTGTATACCTTCTCTCCGCAACCCCA AGCAGCAGAGCTTGACGCTCCAGGAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGAGCTTTGACACACAACTTGA
WI-1936	117 T C	---	---	

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WI-4540	110 A G	GCACCATGTGG CATOC	GACAATGCAGC CATGCA	AGCTTTCTCTTTCTTAAAAATTTGGTGCCATAGTACTGGCTTCTGTGTCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTTGCATTAAGCAACCATGTGGCATOC[AG]GTGCATGGCTGCATTTGTCAGTGC AAATGAGACAACCTTCTCTAT
WI-4582	226 T C	AGCAAGCATCTGCGAAGCCTGGTGACCAGAACATTAATTCACCAACACCACTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTTCAAGCCAGTTTAACTTTATCTCTGTACACA AATACTTTTATGGGAGACAGCATTTGTAATTCAAATCAATAAATGACTCGGTTTGGCTGTACAGCAT AAACAGAACCGTTGGAAATATGGTTT/CCTCTGCTAGAAACCAATTTGAT
WI-1965	105 G C	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	CAAGGTAGTTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTTCAAGGG TAACCAACACCTTTTGGCATTTGAGGAAGTTTAAAG[GC]GAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATCCACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C T	CACGTGTTTCT ATTGACCGTAC TTG	AGAAAAGAG AAGAAAGGAA AAA	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTAGACAAACCCAGAAAAATTAACGGCCTAC CATTTTTCACCTGTTTCTTATTTGACCGTACTTG[CT]TCTTTTCTTTTTCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38 G C	AGTTGTGCTG CTACGTTGT	TTTAAATTTTC TGGGTTGCT	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTAGACAAACCCAGAAAAATTAACGGCCTAC TACCATTTTTCACCTGTTTCTTATTTGACCGTACTTGCTCTTTTCTTTTTCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTGTGACTTTGCTCTGAAGCAGAAAGCACTGTGA CTTACATATTATAGGCCCATCTCTGCTGCTGAAGCCTGCTACAGCAATTTGTAACATATGGCATTGGG ACATATCTCTGAGCCCATCACTATTGACAAAGATTCTCTTTTAAACA
WI-5252	119 A C	GAAATAGGGCAAAATTAAGACTTCAATTAATAAGAAAGTCTTGGGAAAGGATTTGTGATGATCATTC AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTCGTTT[AC]TACCATGTACA TATTATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G	GCAATGCTAG AAAAATTATGC CT	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAATATGATACCCAGGACTGTTGTTCAAGCAATGCTAGAAAAATTTATGCTA[AG]C CAAGTAGACAACTTAAGCAACAGGAGAAAGTTTCTCTTTGTCATTAAAGTCTCTATTTCA ATTACCATTTATCGGGGTAATTAACACTGGAAAGTAAATGCCAGGCTAAATTTGTTAGATTATGATAAT TACACGCTTTTGTATGCT
WI-5257	77 C A	GAGGCATGAA GCAAGAGG	CCAGGGCAGA TGAAAG	CAATGAGAAGTTACCAAGTGCAGGCAAAATTAAGCATATGAAATACCAAGTGTGGCAGAGGCATG AAGCAAAAGAGG[CA]CTTTTCACTGCCCCCTGGTGGTTTTCAGTAACCTGCAACATGCTTTTGCCTCC CGGATGAAAAGATACCCCTTCTATGACTACGCAATTCACCTCTAGGTATGACCCCTAAACATGGGTG GCAAAAT
WI-4649	50 C T	GAGACCATTTCT TTCCGAATG	TGTACTAGGTG TACTTACAGA AATCATC	TCACGTGTTTGAAGAAATTTCTTCTCTCAGTGAGACCATCTTTCCGAATG[CT]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCAGCAAAATTAACAAGTACTTGCTACCTGAAATTTGATTTTTTAA AAAAATCCTCCCAATATTG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGATGTTGGTATTTTCTGGAGAGTCAGTTACTCTCAGTAGATCAATAAGGG GACITGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAACCAAGAAAGTATAAGTTGTCTC TTATAITGCTTTT(A/G)CCAAATCCAGTTTAAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTGGAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAT GAGTTGAAATAAATG(T/C)AAGTTGAATAATGACACTGTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATTTCTGTAGAAAAATTTTACCTGGCAATGATTCAAATAAAGTTTGTCC TCACCTGGAAACTGCTTATCTTGATGTGTCAGTGCATTTCTTTTGTGACGGAAGAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCTGCTGAAGCCATCTG
WI-4722	88	G	A	TGCATATGG AACCCACAC	AATATGGAATC TGCAITTCAGTT G	CTTCCATTCTGCCAGTTAGATGACTGCTCTCCACAGCCTAGAAAAAGATGGGAGATTATTTTC TGCATATGGAACACACACACAG/GA/CAACTGAATGCAGATTCCATATTGAATAGTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAGAGGAAAAATGGAGCCATGTACACAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTGAGTAAATCAGTTTGTGATGGTTGAGATTTCAGAAAAAGTGAATTTTGAAGTAACCATGGG TCAACTATGAT(C/A)CCAAACACAGCAGTGTGCTCTAAAAAATATGATAGTTTCTCTCCTGTCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T	C	TGTTACGTT CCTGTCATC	GGTTGGAAGT CAAATTACCTA GAA	GACTACAGCGCACACAGAGGATTTGTGGCTTGCACAGGTTTGTGTTTGTGTTTAAAGTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAGTTTACTACAGACCTCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGCTCATG(T/C)TTAGGTAATTTGAGTTTCCAAACC TGTTG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGATAGCTCCACATTCGCAGATTCACCACTATGGATAGAAAAATAGTATTTCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTCCAAAGTTATACAGGACCAAGTGTGGAATTT AGCATTTCTGGGTTTGGCATCCATCAGGGTGTAGAACTAATCCCTCA(T/C)GAGAAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGTGGAGGACAAAGAGTTGAAGCAAAAGGAGGAGATCAACTGGG TAGAATAACTCATCGATCCACCCAGGCTCTCCACCATCTCCATCTCTACTCTGAT(T/C) AGGCAGACTTATATGGAATAAAGGGA
WI-2034	150	T	C	CCACAGTGA CC	GGGTAAGAT AGAGTGCAGGT CC	CCACGACTATGTTTTCAGATCCCTGGTACTCACAGAGAGGCTTTGAGGACCATGTGGCGCCCAAGA CCTCCTCTCGCGTTTTCAGTGAAGAAAGATGAATCCTTCTATCTTCTACAGCAGCTGGAGTTCAACA CAGTGCACCAAGGAGT(T/C)GGACCTGCAC(TATCTTTACCCCTTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG

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WI-9014b	44 C T	CCCTGTTCCCATGCTGACCTGTTCTCCCTCCAGTCATCTTTCTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A	TCTGAGAGAAATGACTTGTGGGAGACACCTGCGAGATCCTGATGGGTTGTGACAGACCTGCGTGGCT CAGTGGCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGATCAACATCTGCTAGCGGTCCOC TCTTTTGGCCCCAGTATCATGGCAGGGTTTGTGGACACCTACTAGCTCCCTTCCCATCAACAC A/C/A/CACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C	TCTGAGAGAAATGACTTGTGGGAGACACCTGCGAGATCCTGATGGGTTGTGACAG/C/CCTGGCT GCTCAGTGGCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGATCAACATCTGCTAGCGGTG CCCTTTTTTGGCCCCAGTATCATGGCAGGGTTTGTGGACACCTACTAGCTCCCTTCCCATCAAC CACACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T	CTGAAATCCCTCTCTGCTGCTGCTGGATCGGGGACCCCTTGGCCCTCCCTCTGCTGCTCCAGCC CTACAGACTTCTGCTGACCTCAGGGCAGTGTGCGACCTCTGCGCCTCAGTTTCCAGCTATG AAACAGCTATCTGCAAAAGTTGTGGAAGCAGAAAGAAAGCTGGAGGAAGCGCGTGGGGCCAAAT GGGAGAGCTCTTGTATTATTAATTTGTCGCGCTGTTGTGTTGTTA
WI-9171	62 G A	ACATATCTGAAATGTTGAAAGCCTAAGCCAGGAATAAGAAAGAGTAGAGATAATAATCA(G/A) TCTTTACAACCGATGGTAATTAGCTTGTATTCACAAGACTTCATGC
WI-9174	47 T C T	CTAGACCC ATTCTCTATT	TCTAGAGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGGCCAGTCTAGGACCCATCTCTCTATTATTCAGTCTGCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCACTATGGTCAAAATTGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA	CAGAGTCTTG AAATACAGGG A	AAGGCCAGATGCATCCCTGGAAGACATCCATGTTCCGAGAAGAACAGATAGATCCCTGTATT TCAAGACCTCTGTGCATTTATTATGAACCTGCGCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGGCGGTTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A	CCACTTCTCC CGCA	AAAGGAAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAAACAAAAATGGCATCCCTGTCAAAATGGAGTCCACT TCTCCCGCA(G/A)ACCTAGGTGACAGCTTTCCCTTTCATCTT
WI-9193	94 G A C A	AGAAATTGT CTGCCTTAAAG CA	GGTGTGTGTGG TAGGGGG	TTGACAACCTAGAAATTTCTCCCTTATGTATCTCTATCAATTTGTAGCAATTTGACAGAGATAA CTCAGAAATATTGCTGCTTTAAAGCA(G/A)ACCCCTTACCACACACCCCTGTCTCTC
WI-9015	48 C T	TTTGATTGATATGTTGAATCTCTCAGCGAGAAATTTGGCTGGATTGCTGCTTTGGTTAATACAT CTTCCCTAAAGAGATACACAAAAATCCATCCAGGTAGCTCGGACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGACACAGAGGCTGTGAGAGAGGAGCCAGAGTCCCTAATGACACCCACTCTAGCC CTGAGGCTGTGCGCTCAGACTGGGGAAGAGTCCAAAGGAGGAGGAGGAGCCACTCTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 GC	CAGTCCCCCA GATTGA	CACITGCCAC ACTCAGAC	GTACCCCTGTGAGGTCCGCCAGATTGAGCTGTGAGTGTGGCAAGTGTGTCAAAAGGGGCG TGCCCCCAGGAGATGAGGCTGAGAGCAGGAGTGTGAGGCCGAGAGTCA
WI-7836	120 T C C	CAAATAACA ATGCAACGTTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAACACTCTCATTCAGTAGTTACTGAAAGAAAACCTCTGCTA GAATGATAAATGTCATGGTGGTCTATAACTCCAATAAACAATGCAACGTTCCCT/CJGATTTCTAAT CTTGGTTCTGAGAGCCATTGGTTTTCAGTTGTAGCAATCCCATACAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAAGTGACAG TAA	AAACAACTTA ACCAGAAAGCT TTAA	TCCATTCCCTTTGGCCCTGCAGCATGTCTGCTCCAGAAATTCAGCTTCAGCTTAACCTGACAGATTC GTTAAAGCTTTTCTGGTTAGATTGTTTTCATCTGGTGATGCTCTTTTCCATGTGTACCTGTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTTT T	CCCAATTTTAA TTAAAGTTTAA CATCTAT	CAAAATCTTGGAAATATCTCAAAATGTTAAATAACAATATGAATTTTCTCATGTCATATTAATACTACT AAGCATGTACGTGAATTTTAAATTTGTTATAGATGTAAAGCTTTTAAATAAATTTGGGTGTGG GAAGATTAAAGGGGGGTGTCTCTGTGGTCTCCCTCCCTGCCCCCA/CAGTGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGAACCTGACCACTACTGGCCCTATGGGTGGGGGTGGTAGGCAGG TGAGCGTAAGTGGGGAGGAAATGGGTAAAGAGTCTACTCCAAACCTAGGTCTCTATGTCAGACCAG ACCTAGTCTCTCTAGGAGGAAACAGGAGACCTGGGGTCTCTGGAT
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA TTC	GCTTGAGTGT AGTCTCGCAGA	CAAGGGTACCTCCAAACATAATTGATTCTGATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATAGTGGGGAGGCGCTGGCTACTGTCTCTGCACTCTGCTGCTTTG CACACTTGTCTTCTTCACTGCTGGAGTCTCTGGAGGTCAGGCTGGGGTAAGCCGGGGTTCACACA GGCCCGACCCCTGGCAGGGGTCTGGCCCCCAGGTAGCGGAGAGCAGTCCCTCCCTCAG/GTAACT GGAGAGGGGACTCCAGGAATGGGAAATGTGACACCAACCATCTCTGAAGCCAGCTTGCACCTCCAGT TTGCACAGGGGATTGTCTGGGGGCTGAGGGCCCTGTCCCCACCCCGGCG
WI-7307	128 G T	GAAATGTGAC TTCACITTTGGT T	CAGGTAGAATT TCTGTCCATT G	GAGGAAATGTGACTTCACTTTGGTGCTCAATGGACAGAAAATCTACCTGTGTACATAGGAGAA GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTGAGGTGGAAA AATCCCTTTCTGGTAATCAGGCACATGATGAACCTTGAATTAGTGGTCTGTGATTAAAGTCTTAAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGGTAGGACCTAAATTCCTTATCATATCTTTAT AATCAGCCAGTGTATCCACAGTTTTTGTATGTTTAAAGTAACTTATCTCTGGATTTCATG AAGGTGAATATCGTTTGTAAACTGAATAGAAATGTATAGCGATGA
WI-9274	25 C T G			AATCCCTTTCTGGTAATCAGGCACATGATGAACCTTGAATTAGTGGTCTGTGATTAAAGTCTTAAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGGTAGGACCTAAATTCCTTATCATATCTTTAT AATCAGCCAGTGTATCCACAGTTTTTGTATGTTTAAAGTAACTTATCTCTGGATTTCATG AAGGTGAATATCGTTTGTAAACTGAATAGAAATGTATAGCGATGA
WI-7313e	266 T C			
WI-7313c	256 C T			

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGAGCACTAGAGAGGAGGGAGAGAGAGAGAGTTAGAGAAAAAGCCACCGGAGGAAAGG AAAAAATCGGGCAACCTAGAAACGTTTTCATTCGTCATCCAGAGAGAGAGAGGAAAGAAAA [T/A]ACAACTTTCATCTCTTTGACACGTTTCATAACATCTACATA
X86400	118 A C			TCCTGCAAGAAGTTCTCAAGCCCTTTTGATTTTGTGCAATAAGTACAGCTTTGCATAAGAGTGAAA TTGGCTAGCTTAATGATGATCCATAAATCTCTCTAATTTTAAAGTGAGAG[AC]CTCTTTTAAACACCT GTTAAATTAATGATGAGAGCTGAGAACTTAAATTTATGTACCACCTGTTTATTTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTTCA
WI-8053	242 T A			GTGGCCACTACATGTTATAGAACCATCATCTTTGTCACACAGCACAGTCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAGAGTGTCCCATTAAGAGGAGCTTTTAAATCAACCTAA TAACTCTAATTCGCTGACTTTTAAAGATCTAAGGTCAATTTTAAATACATGCTGAAAGGGTCACA ATTAATCTTTGATCTTTTACTCAGTGAATTAATTAAT[AT]TCAGAAC
WI-6190	165 G A			TACACAATGAATTCCTTTTATTTGGGTATGTCATCCACATTTTCAGCATTTAGTGGTCTGCAACAGCAAG TGGAAGACGACGCAATTTGCCAGGAGTCAAGCCACCAATTTCCGGGATCTGCTGTGCAACCCGG GTTCTCTTAATCCCTGCTGAGGATCTTTG[A]GAAGCAGCAGCAGCACCACCAAGGCGATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAAACTAGACCCCA
WI-6275	148 G C			AACAGTCAACCAACACATGACAACTCGCCAGGCAAGGCTTCTCCCTCCCTCTTTCGCTGCC ATGTGCTAGTCAAGAGTGGGGGAGCAGGATGTTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAAAG[C]GGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCATTAAAACTG ATTGCTTTCAGTAACTGGTATGCTGAA
WI-6421	41 G T			ACCAAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGTTGTTGGGCTTCTGAAAGAAACCTTGC TGACAGCTCTCACTGACCTGACGACGAGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACAATA GAATTTTGGGGCAGAACCTTGAACCTGGCCACAGGAGACATCCCAATATCCCTCTCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T A			GGGTGAGACGGGTTTATTTGTCACATTTACACAGCGTCAAGGCTGGCGCTGGCAGCGGCTGCTC CTGTGCTGGGGCTGCTAAGAGGGCTTCACTTTTTCACCACTATGTACAGTCAGTGGCTGCTCAA GGTATGGGCTACAGTCTGCATCAGTGAGTCTGTACACACATTTTACATAAATTACACAGCACTC ATACATGAAAAA[T/A]AGAGCCTAAGGGCTGTATTTTAAAGAAAAA
WI-9420	202 G A			AACTGTTTACAAAAAGGCTTTGCAAACTTCACTACTGAATTTGAAAGTCAATGACTGTGTTGTTT TAAATAATGTACCAAGGAATACAAATTTGGATAATGATCATTTTTCATGCTCAGGAGAGAAACAGCAG AGAAATAAGGATACGCAAGGTTGCAAGGAAACCGGAAACCCATTGTGTACTGTCTTCACACAG [G/A]GCATCTTTCTCACCTTAACCTGACGCTGTGCAAGATGCTCAGTGTG

WI-9448	184 GA	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGCAGCACTAGTGAGAGGAATACTCTGGAGAGAGAC TGCCCTTGCCCATGGTGGTTAACTACATAGAGGGGACTGAAATCTCTTGGATGCCAGTCCAGATCC TTTCTAAGAAAAATGGGCTTGTTGGTTCCAAGGCTGAGAGCTGGCACCAQ(G/A)CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAGCGCATGTTCTACGTGCCGGTGAGCAG
WI-9470	204 GA	---	ATGTCAGAGAGACACAGACAGAGGATTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAAGAAATAGATCTCCCTAAAGCCAGATTCCTCATGAGCAGCGCTGGGACACTGATGAC AA(G/A)GC AATCAACTCATCTCTCAAGCTCACAGGGCTCACTCTCCCAAG
WI-1245b	201 GT	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTCTAAGCCCTATAAGGAAGAGTAGGTGTTAATGGCA TCTTAGGGCAATGGTAGTGCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGTGGT TTATTAATTCATTTATCATCTGGACAGCCCTTCTTATAAGTACATCCCTTGCCTCTCTGAGGCG/ TCTAAGATCCCAAGGTGGCTCTGTATCCAGAAA
WI-1245a	85 TC	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTCTAAGCCCTATAAGGAAGAGTAGGTGTTAATGGCA TCTTAGGGCAATGGTAGTGCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGGT GGTTTATTAATTCATTTATCATCTGGACAGCCCTTCTTATAAGTACATCCCTTGCCTCTCTGAGGC GCTAAGATCCCAAGGTGGCTCTGTATCCAGAAA
WI-1031	149 GA	---	TTCAAGTAAAGGACAGGTCTAGAACAAAGCGTTCCCAACCCCTGGCAACATGACAGATTTGGACCAA TAACTCTTTTTCAGGGGACTGCTACACATTTGGGATGTTTAGCAGCTCCCTGGCTTCTACCCA CTAGATGCCAGCA(G/A)CACAAACACCCCTCCCAACAAATCATGACAATGTAATGCTCTTAGACAT GCCAAATATACCTTTGGGACAAAATGGCCCTGATTTAGAACCACTGGTT
WI-5385	110 GA	---	AATGAGTCATTTGGAGTTAGAGGAGGTACTGAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCGATAATTTAACATATGGTTCTGCCAGGAATCG(G/A)CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGATACTCAGTGACCCCATGGCTAGAGTTCCTGAC COCTGCTACGGGAAACATTGAATGCA
WI-5403	199 TG	---	ACCAACCGTTGGCAAGGCTCCCAAGACTCACCCCACTTTGGTGTCTTACCTATGCGGGGTG GGATTTGAAGAAATAACCATAAATATAATTTGCTACAAATTTTCCAGTAGTACCAGGCCAGCCTAT TGGAAGAAATCATAAATGACCCCTACAATGATTTGCTCTGGCTTGGTCCAGGCATAGAGTTTG TGGCCTACACCCCATTTATCATTTGAACCCCTCAAGAGCATCCAGTTGGGGCT
WI-5801b	157 GA	---	TGGTATTTTCTCTTTTCTAAAATGTTATGATTAATTAGTGTCTTTGTAGAATTTGAAAAATGTAAA TCAGAGAACAGAGAAAGAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGCCCTAG GGAAAGAAAGAGAGCCCTGGGA(G/A)AGGGAATGAGAAAAAGCACACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAATTAAGT

WI-1968	167 A G ---	---	---	TGGTGGAGAGCTGAAGGCTGAAAGATAGTCTGCTCTGGTCTTCGTTGGAATGGATGAGTCTCT TTTACAAAATTTTCTCTGCTGCCATGGGTGTTATGTTTGAATCATGGAGTTGGAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAACITGAGCAAGTGCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCTGTAA
WI-4701	198 GA ---	---	---	GGGTTCATTAAACAGCCTTCCACTGGTCTCAGATTGACGGGAGATGTAATAAGGAAGATAG AAAAATGGTGGCCCACTATTGACTTGATACACCTACAAACACACATTAAACTCTCCCACTCTA CCCGCAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATCTATTTCCCAATTAGAG/GA CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	---	TTTATCTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCTTTAATTA TGCACCTACTGTGTGGCTACAGACATTTCTTCAATTTGTAATTTCTTAAACAGCAAGCATAACT GATGTGTCATCTTTGTTATTTCTTAAAC/AJAAAGAAAAGTCTTTTGTGCATCTGCCCTCTCTGT CTCTCTGTTTCCACTCTCTGTTATTTCCCTATTCCAGCATTCATGATTA
WI-4860	72 A G ---	---	---	AAAAAACAATTCATTGACATTTAAGAGATTAAGAAAACAAACGATCCACTGTGTGTTGCTT GATTTA/GJGGAGATAAACCTGATCTCTAAGAAAATTAACCAAGCAGTACACTAAATAGCCT TTGTGTGGTTTTCAGGAAGAAAGCCAACTCCAACTAAGTTGCTAAGAAAATTAATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAAATATAGCA
WI-9705	111 C A ---	---	---	TGAAAGGACCAGTTTGAATGCTTACCAAGGTAAAGTAAATCGGAGGGGAGGAGTAGGAGTTGCTT CCGGATGTGCAATAATTCAGGTCTTTAAGGAGTTCCGCTGCQC/AJAAAATTTTAAACACTGATGC TGTCTACAAACGCACATAGAAATCGGTGTAGATTGCGGTTCTCTAGTAGCTAATGTTTAGATA TGATTTGTAATTTTGTGCTGTGTTCTTGGTG
TGR- A004248	177 A G ---	---	---	CAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTCATGTAAGGGTGGGCGAGGTGGACTG AAGATCTGTGGCAGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTCTATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCTACAGCCACAGAG/GTCCCTCCAATTTAGGGGCTCC GTGGGATGGTGGAGCCAAATGAAGCACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	---	GGGATCAATGTGTGTCTCATCCAAATAGCACT/GJCATGACCTCAGCCCATCTCTTCTTCCC TATGTTCCAGAGACAGAAATAGACCTGGCCCTTCTCTAGGGGATCAATAATTTGGAAGGATGAG GACTCCAAAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTCTGGGATCAATTTCTATGGAGCC TGGGGAGAGGGATCTTCTAGTTGA
WI-7747b	88 T G ---	---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAATCTTCTTGGCCTGCTTCTGTTAACTGTATGTACATA TATATATTTTAAATTTGTTT/GJAAAGCTGATTTACTGTCAATAACAGCTTCATGCCCTTGTAAAGTT ATTCTGTTTGTGTTGGGTATCTGCCAGTGTGTTTGTAAATAGAGATTGGAGCACTCTGA GTTTACCATTGTAATAAAGATATAATTTTATGTTTGTCTGA

WI-7747a	44 T C	GTGAGGGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTTCCTGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTGCAATAAAGCTTTCATGCTTTGTAAAGTT ATTCTGTGTTGTTGTTGGGTATCCTGCCAGTGTGTTGTAAATAAGAGATTTGGAGCACTCTGA GTTACCAATTGTAATAAGATATAATTTTATGTTTGTGTTCTGA
WI-7189	197 T C	TCCAGAAATTTCTCTTCAGCTCAATTTGTCTCTCTCAAAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCAATTAATTTCCCTTCAACAAATAATAATTTTACAGAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAAACATTTTTC/JAG TTTGCAATAGAACTAATAC TGGTGAAATTTACCTAAACCTTGGTTAAT
WI-7850	57 G A	AGCCCCAGCTGGACTCATGGATGTGACCCCTTGTCCCTGCTCTTCTGCTCTGGG/GA/CTCATGTA TCTGGCAGCTCTGTGACCCCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCTGCTGCTGAAGCT GAGAAAGCAGGGCAAGGAGGAGGACAGAGCCCTCAGCCAGCCAGGATCCGCTCCTCATTTT ATTGGTATGATGAATGGAAATGAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69 G C	CTCTCTCTTCATCCCATCACCCCTAAATAGGTAGGTAGGAGGCTGGGAAGAGGTGGGAGGAGG G/G/JAGAGTGAGGAGATAGGAAGGATTAACCTCTCTGTGTTATTTTAAAGAAACATTTGTT GGTGGCAGCAATCTCCCTGCTCCTATCAGCTGTAGAGGCTAATTTATCTATAATAATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAAATTTGTCAAAATTTAAAT
WI-7919	242 T C	GAAGCAGCTGGATCACTTCCCGAGTCTTGGGAGCGCTTGTGTGGAACACGAGAGCTCCTCT CAGGGCCTGGCAGCTCACCTCTTATCTGTATGATGTTTGGTTAAACACTGTCAATAATAGAGAT GTGCCAGATTAGATTTTCTTACCTAATCTGTTTAAATTTGTAACCTTTATCCATTTGAAAGTGCA AGCCCAATCAGATAAGCTATAATCTGGTCTTTAAGGAATTCACAACTTT
WI-7928	101 T G	CTCCCTCCTATGCTCTCAGCAGCAGCTTGGGCGACACTTGTCTCTGACCGTTTGTGGGCTA TTCCCTTGCAGTGCAGACATCGTCAAAATTCAT/GJACAAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGGCACTTTAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCATTAATAAATACGTACATTTTCAGGTAATGGTA
WI-7936	131 T A	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTAATATATACATCTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCAACACCTTACACCAAACTTAJ ACTGAATGAAGAAGTATTTGGTAACCGCCATTTTGGTGGGAATCCAAAGATTGCTCTCCCATATG CAGAAATAGACAAAGATATATTAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99 T C	TACAGTTCCAGCCGTTGCCACTCATCTGCGGCTTTCCTTTGGTTGGGGGCGAGATTGGGTTGG AATGCTTTCCATCTCCAGAGACTTTTCATGT/GJAGCCCCAAAGTACAGCCCTGGACCCCTGGTGTG TGAGTAGTAGAATACCCCTGAGCTGAGCTGAGCCCTGAGCCAAATGGGACAGTTACACTTGACAGAG CAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-276	25 A G ---	AGCTTTTGAATCCAAAAACACATAGCTTGACTCTCTTATCTCCTCTTGTGTAACATCTATCC CTGAGGCGAGAAATACAGAAACCCCTGTGGCTGCTGAAACGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTTATCCTCTCTGCTATCCTGATGACTGGGCAAA
WI-427	59 GA ---	TTTTCCCAATCCACAGGTAAACTAATAATGATGTATAGAAATTTAGAACTACTTCGAG/AGTTT TTTCCCTGGGGAATAATCACAACCATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTATCAGACAGGTAGAGCCCTGACTCTGGCAGGATAGCTACCACTAGCTGTGAGACTTTATGT ATTCAITTTATAGAGCCAGGGTCTTGCTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	CTCTTCACTCCAACTATATTGCTTACTTAAATGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAA/CTCAAATGGTCTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTAGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATACTCTCCACTTCC
WI-562b	106 T C ---	CTCTTCACTCCAACTATATTGCTTACTTAAATGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAA/CTCAAATGGTCTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTAGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATACTCTCCACTTCC
WI-562	103 T C ---	CTCTTCACTCCAACTATATTGCTTACTTAAATGTTACAGATTAAAGCCAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAA/CTCAAATGGTCTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTAGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATACTCTCCACTTCC
WI-597c	141 A G ---	GTGTAATTTGGTGGCTTTGCACTTTTCCACAGTAACCTTTAGAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATCT GATACATG/AGTAAAGACCCCTCCAGCTCTGGTACCTCATCATTACCAATGTGAGAAATTTAAAC TTGATCTAATATCTTCAACACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	GTGTAATTTGGTGGCTTTGCACTTTTCCACAGTAACCTTTAGAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATCT GATACATG/AGTAAAGACCCCTCCAGCTCTGGTACCTCATCATTACCAATGTGAGAAATTTAAAC TTGATCTAATATCTTCAACACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	GTGTAATTTGGTGGCTTTGCACTTTTCCACAGTAACCTTTAGAATNNAAGGTGGAAGGTAAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATCT GATGICATGATAAGACCCCTCCAGCTCTGGTACCTCATCATTACCAATGTGAGAAATTTAAAC TTGATCTAATATCTTCAACACTAATATACCTGAGAGAAATAAGTCTATTTAAT

WI-811	66 G C	TTCAAAATTAACACCATTTGGGTATATTAATAATTNGCTCTATCCATAGTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGCTCTTACGTATTACGTATTCAGTATCGATCATGCCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCACCCCTACTTGGGCTCTGACTTCCTTCTCTGGGCT GAACCTTCTCTGTGTGCTGTCCGCTTCTCTGCTGGCTGCTCCATAC
WI-81b	156 A G	TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTACACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCCGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCTATGGTTT
WI-81	156 A G	TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTACACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCCGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCTATGGTTT
WI-867b	119 G A	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCAGTATCTGGCAGTCTTCCCTTTTCACTCCG/GAJTTGTGTTGGC CAAATAATCTCCCCAGGGAGTCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
WI-867	113 A G	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCAGTATCTTCCCTTTTCACTCCG/GAJTTGTGTTGGC CAAATAATCTCCCCAGGGAGTCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
WI-867	119 G A	AATCTTAACAGCCCTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCAGTATCTTCCCTTTTCACTCCG/GAJTTGTGTTGGC CAAATAATCTCCCCAGGGAGTCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
WI-871b	123 C G	TCATCAGACCTGAGATTACGATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG/C/GJAAGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCAGTGTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTTAACCCCAATATGNCCTGATTGTACATAA
WI-871	123 C G	TCATCAGACCTGAGATTACGATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG/C/GJAAGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCAGTGTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTTAACCCCAATATGNCCTGATTGTACATAA

WI-884	198	T C	AGGTTCTGGACTGTGCTGGGAACAATGGGTCGTGGAGATTCCTATTTTGGATTTTCACAGAT CAGTAGAGCCAAATGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTTCTGTATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTTAATCATGGACAACNNAAAAGGAATATTCG ATCCGCGATGCAACATTTATTAGTGAAACATGATGAAATGAACATAAT
WI-921b	205	G A	CACCTCCAAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTTCACACTGACTGA TGCTTCTGCGAGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGAGCAGTTATCTGG CAGTGATGCTCTCACGCTGCCCCCAGAAAAGTTCTTNGCCAGGAAAAGCAGCATCCATCTAC TCGTA/GGGAGAGATCTGACAAATTTAATCAGGAGGAATTTCTCCGAG
WI-921	205	G A	CACCTCCAAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTTCACACTGACTGA TGCTTCTGCGAGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGAGCAGTTATCTGG CAGTGATGCTCTCACGCTGCCCCCAGAAAAGTTCTTNGCCAGGAAAAGCAGCATCCATCTAC TCGTA/GGGAGAGATCTGACAAATTTAATCAGGAGGAATTTCTCCGAG
WI-945c	90	G C	GGCTGGATGAGAGGTCTACTTGTGTGCTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACAGNGATTGGCTAACG/CATGCGATGCGAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACANTAGGTGCAGCANNNGGTT TTCTGTGTCATAGAACTCTTAAAGGGGAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90	G C	GGCTGGATGAGAGGTCTACTTGTGTGCTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAGNA GAAAGACAGNGATTGGCTAACG/CATGCGATGCGAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACANTAGGTGCAGCANNNGGTT TTCTGTGTCATAGAACTCTTAAAGGGGAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167	C T	TTGCTTCAAGAAGTTCTTGTCTCAGGAAGTTTATTCATTCAGCAACCTAAATTTGTTTGGATACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTACC CTGAGGAATTTATCAAGATGTTAAGTTATCTTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A	TTGCTTCAAGAAGTTCTTGTCTCAGGAAGTTTATTCATTCAGCAACCTAAATTTGTTTGGATACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTACC CTGAGGAATTTATCAAGATGTTAAGTTATCTTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C	TCCCACTGAGTATGGCTTCAGTAGTTTATTATGATGCGCTAGGTACATTTGTTTATTGTTCTG CGAATGTTGTTATCTTGGGAGAAATGCTCAACTATAAATTTGCTTCTGACCCCTTTCTGTGTT CTTCTAAAGATACAAAATAAATGTAACATTTAGACCTCTCATAATTCGCTGTTTACTCTCCTCG ATTTTTTCCATTATTTTATGCTCTGGCTTCTTTTGTAAATNTG

WI-1147b	204	G A	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCCAGGGTTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTAACTGTATGACTTCTATCCAGCCACCGCAACTTCTCCTCTCCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACCTTGTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAACAACCTCTCATCAGGCAGA
WI-1158b	147	C T	GCATTGAGGGTTCGTTTAAATGACATTCTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GCCAGGT TAAGTCTGGGG/C/TTCTGGGGTCAGGCTGCTGGGTACATCTGCTGCCCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G	GCATTGAGGGTTCGTTTAAATGACATTCTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCCCTGGGTACATCTGCTGCCCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C	AAGTTTACAGAAAAAATACAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAAAACATATGCCCA TCATCTTCAANGTNCACAGACACTTATCCCTGAGCAGCCATTTCTTTTGAATGNT/C/JGNCANT AAAAATGATTTGAAATTGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202	C T	TTCTCAATCCAACTGTGTGTACTTTTATTCTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTAACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTTAANTGNNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCCTACCA
WI-1305c	46	C T	TTCTCAATCCAACTGTGTGTACTTTTATTCTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTAACCAATTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCCTACCA
WI-1305b	153	T C	TTCTCAATCCAACTGTGTGTACTTTTATTCTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTAACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCCTACCA
WI-1305	202	C T	TTCTCAATCCAACTGTGTGTACTTTTATTCTTCTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTAACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTTAANTGNNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCCTACCA

WI-1341b	136	G A	---	---	TATCAGCATGATTGGCTGTGGACACAAGTCAATTTGACTTTTGTGNNNTCTTTCTTCTTNTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAAATTTGGCTTNCCTTTTGTNAATTAACCCAGC [G/A]GGATTGTGATGGATCTGTTATTTCTCTGTCTTGGAAACAGAGAGTCTCTCTGNGAGNTG GTTTCAGGAATTTGCTCTGTTCCCGAGCCACTTGCACITAGCAAGTGT
WI-1349e	192	G C	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGAATGCAGGCGAGGTGAGGTGCTGGCCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1349d	264	C A	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGAATGCAGGCGAGGTGAGGTGCTGGCCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1349c	192	G C	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGAATGCAGGCGAGGTGAGGTGCTGGCCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1349b	264	C A	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGAATGCAGGCGAGGTGAGGTGCTGGCCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1349	264	C A	---	---	CTGACAAATGTCATATCTCACTCTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGAATGCAGGCGAGGTGAGGTGCTGGCCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAATA
WI-1403b	57	C T	---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAAGTTCATTTCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTACATCAACATAATTTCTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58	T C	---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAAGTTCATTTCCGAAT TGCACCTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTTCTGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1803b	77 A G	...	CCACTCAGTAATAGTGTGGAGTAAGTATGGTAGGCACATAATAATATTTCCAGGCAGAA CCATTATGATGAGTAGGTAGGCATCACACTTGGGAGGACATATCTGGAGTAGATATCCTG GGTCTAATTTCAATATATCTACTAAGCATGACTTCTAGAAAATTTACTTATTACTCTTGCCICAA GGAATGGGAATACCTATAATACAGCTTATTGAGGAAATAACTGGAAATCA
WI-1837b	112 C T	...	TTACTTGGGATTTTTCATAGCTGATCATAATTTACCAITTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAACCCGTTTATACIC/TTCGTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACTTTAGCTTCTGCTGGCT
WI-1837	112 C T	...	TTACTTGGGATTTTTCATAGCTGATCATAATTTACCAITTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAACCCGTTTATACIC/TTCGTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACTTTAGCTTCTGCTGGCT
WI-1840b	79 G T	...	TCACCTAGGGAGGTCGCTAAAAATGAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TGAGAAATCTGAATATTCAGCACATACAAGTGTGACACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTGTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T	...	TCACCTAGGGAGGTCGCTAAAAATGAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TGAGAAATCTGAATATTCAGCACATACAAGTGTGACACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTGTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T	...	GGGCTCACTTTTCATCAGAGCACATATCAGTGATGCTGTTCCTTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTCTTTGAGGTAAAGGACCTGCNNTTTTAC/TGTC/GCNAATAAACTCCCAAAA AAGTGTAGTCCACAGGTTTAAATAGTCTGTTGAATGAATTTCTGTGCGACCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T	...	GGGCTCACTTTTCATCAGAGCACATATCAGTGATGCTGTTCCTTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTCTTTGAGGTAAAGGACCTGCNNTTTTAC/TGTC/GCNAATAAACTCCCAAAA AAGTGTAGTCCACAGGTTTAAATAGTCTGTTGAATGAATTTCTGTGCGACCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T	...	TGTTCTCTGGTCCAGGACCGGCTAAGTCTGTGTCATATGAATAATCAACTGCACAACCCGNG CTNAGGTAGGNTACCTNGGCAATTGCCCATCTTACAGCTGCAAAAGAGGCTTCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGAGCGCAACAGGTGTTTGAACCCAGCTCTGCT GACTTCAGATCTGTGCTTAAGTGGCATGAGAAACCACTTTCTTGTCTCC

WI-1900	119 C T	TGTTCTGTGTCAGGCAACCGGGCTAGTCTTGCTGCTAATGGAATTAATCAACTGGACAAACCCONG CTNAGGTAGGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGG(C/T)GCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACTAGAGAGGCAACAGGTGTTTGAACCCAGCTCTGCTC GACTTCAGATCTGTGCTTAACTGCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165 C T	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACCAAGCC(C/T)CTCTGAANCCTGGGTCCACGTTGGAGATAGTAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165 C T	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACCAAGCC(C/T)CTCTGAANCCTGGGTCCACGTTGGAGATAGTAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164 C T	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTGGAGTGGGATCTGGAGAGCACCCCT GCAGAGCTTCATCTGTTTCAAAAGTGCCTATGCANGTCTGCTGGGTGTGGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAACTTAAATATGCACCTCCCAACTTT
WI-1960c	270 A T	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTGGAGTGGGATCTGGAGAGCACCCCT GCAGAGCTTCATCTGTTTCAAAAGTGCCTATGCANGTCTGCTGGGTGTGGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAACTTAAATATGCACCTCCCAACTTT
WI-1960b	270 A T	CTGATGCCAAGTCAGCTTAGAGTAAAGGAAATCCAGAGAAAGTNTTGGATCTGGTAAAGTAGGATCA TTCTGGGCAATTTCTCATAGAGTNTTGTGTTAGTCTGCTGTAATAATAGTGTGCCCTAGGAAAGTTGT TTCTGCTGCTGCTGTGAAAGCCCTTCCCATCGAGTATAGTACTTTCAGTTATGGAGATTTT /CTAACAAATCAACACTGGCTGAGGCTGTTGG
WI-1977	203 T C	AAATCTAGAAGCCAGAGTCAGCTACGATTTATAAAGTTGAAGTAAATGCATTTGAGTTTCATGT TTTCTCTTAAATTCGACAAAACCTAGCTAAAATCT(C/T)TTTAAATCAGTTACCAGAGGCAATACCT GGGTAAATGAAGCACTAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACTTTTTTCTACTCTCAIT GGCTTCAACCAATGCTTCCACTGGATC
WI-2012	102 T C	GGCTTCAACCAATGCTTCCACTGGATC

WI-2013	127 C T	---	---	CTTTAGAGGTGGTCATTCGGTCCCTCTCGAAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACGACACTCTCTCA CCAGAAAAAGAGAAATACCATCATGAGGAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCAGCTTCTGAGCCCTGGTACTGCAATCC
WI-2032c	166 G A	---	---	ACCAGACATCCATCAGGAGTTAGTCTCTGCGAAGCCAGCCCTGCCCTTCTGATTTCCAAAAACC TCAATTTTCTTACTTACTCATAATATGCTAGGATATCCACATAACCAAAAGCCAAACCTTAACC ACATCACCCTGCTTTCTAGATGTACACGATGTGGGACCTCTGCTCAACCTCCGACTTTCACAGA AGATCATGGTTAGGCTCACCTCTCTGTAATTCCTCTGTTTTCAAAGGG
WI-2032b	219 C G	---	---	ACCAGACATCCATCAGGAGTTAGTCTCTGCGAAGCCAGCCCTGCCCTTCTGATTTCCAAAAACC TCAATTTTCTTACTTACTCATAATATGCTAGGATATCCACATAACCAAAAGCCAAACCTTAACC ACATCACCCTGCTTTCTAGATGTACACGATGTGGGACCTCTGCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCACTGCTCTCTGTAATTCCTCTGTTTTCAAAGGG
WI-2032	219 C G	---	---	ACCAGACATCCATCAGGAGTTAGTCTCTGCGAAGCCAGCCCTGCCCTTCTGATTTCCAAAAACC TCAATTTTCTTACTTACTCATAATATGCTAGGATATCCACATAACCAAAAGCCAAACCTTAACC ACATCACCCTGCTTTCTAGATGTACACGATGTGGGACCTCTGCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCACTGCTCTCTGTAATTCCTCTGTTTTCAAAGGG
WI-2054b	188 C T	---	---	CGTTTTCTTACATCTGGGACATATAAGANGAAGAGNAGCTGCTCTTCTGTTGTTAGTTTGTCT CAGAGCTGCTTAGAGCNAGGACAGACAGGTCACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCAGCCAGGCTCAACAGAACTAATACCTGCTTCTCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGCTTT
WI-2054	183 T C	---	---	CGTTTTCTTACATCTGGGACATATAAGANGAAGAGNAGCTGCTCTTCTGTTGTTAGTTTGTCT CAGAGCTGCTTAGAGCNAGGACAGACAGGTCACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCAGCCAGGCTCAACAGAACTAATACCTGCTTCTCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGCTTT
WI-2573d	129 T C	---	---	TGGGATTAACCCCTGTTTCTCTTCCAGTTCAGTGTGCTTAAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGACCTTGCCGTTTCAAGGTTTCCGCTTTCTGCTGTA TATCATCTGATCTTCCCAACAGGGCTTATATGCTAGGTAAGGGGTAAGCAACAGAGGCTGTGT GAAGTAAATGATTTGCTTGCAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C	---	---	TGGGATTAACCCCTGTTTCTCTTCCAGTTCAGTGTGCTTAAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGACCTTGCCGTTTCAAGGTTTCCGCTTTCTGCTGTA TATCATCTGATCTTCCCAACAGGGCTTATATGCTAGGTAAGGGGTAAGCAACAGAGGCTGTGT GAAGTAAATGATTTGCTTGCAAGGTCATATGGCTGGGCTTGGACGAG

WI-2573d	129	T C	---	---	TGGGATTAAACCCGTTTTCCTCCAGTTCAGTGGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTTTCGTTTTCGTTGA TATCATCTGATCTCCCAACAGGCTTATTTATGCTAGGTAAAGGTTAAGCAACAGAGGCTGTG GAAGTGAATGATTTGCTTGCACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C	---	---	TGGGATTAAACCCGTTTTCCTCCAGTTCAGTGGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTTTCGTTTTCGTTGA TATCATCTGATCTCCCAACAGGCTTATTTATGCTAGGTAAAGGTTAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165	A C	---	---	TGGGATTAAACCCGTTTTCCTCCAGTTCAGTGGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTTTCGTTTTCGTTGA TATCATCTGATCTCCCAACAGGCTTATTTATGCTAGGTAAAGGTTAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129	T C	---	---	TGGGATTAAACCCGTTTTCCTCCAGTTCAGTGGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTTTCGTTTTCGTTGA TATCATCTGATCTCCCAACAGGCTTATTTATGCTAGGTAAAGGTTAAGCAACAGAGGCTGTG GAAGTGAATGATTTGCTTGCACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60	A G	---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAAATTTACAGACATTAAAGCAAGCTTTCG/GJCTC CCACTTCCCTCCCTCCACTATCACCCTCAACCTTCCATCCACTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAAGGCTTCCCAATGATGACGCCAGTTCGCATACAGTTTGTA CAGAAATGCTATATTATGGAACAGCTGAAATGAAATATCGATATAC
WI-2868	60	A G	---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAAATTTACAGACATTAAAGCAAGCTTTCG/GJCTC CCACTTCCCTCCCTCCACTATCACCCTCAACCTTCCATCCACTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAAGGCTTCCCAATGATGACGCCAGTTCGCATACAGTTTGTA CAGAAATGCTATATTATGGAACAGCTGAAATGAAATATCGATATAC
WI-2870b	131	T C	---	---	CATGCTGTGAACCTCTGTGCTGCTGCTGCTGGGAAATTAGAGCAAGGAAATGTATATCTAGGC TTCAAGGAGCTTCTCATCTCATTTAGAGGAGACAAAGATGAACATCAGGAAATGACTGGATATGAT/CJ AGAAATGAATAGAGCCCATTTTAAATATATACAGCTTTATGTCACCTTCCCTTCCCTGCGCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870	131	T C	---	---	CATGCTGTGAACCTCTGTGCTGCTGCTGCTGGGAAATTAGAGCAAGGAAATGTATATCTAGGC TTCAAGGAGCTTCTCATCTCATTTAGAGGAGACAAAGATGAACATCAGGAAATGACTGGATATGAT/CJ AGAAATGAATAGAGCCCATTTTAAATATATACAGCTTTATGTCACCTTCCCTTCCCTGCGCATCAC TGGGCTTTTACAAAGGAGGCTTT

WI-2954c	49	T A	---	TTAGCACATATCTGTGTGGGACTTAAGTGAGACAAGGCAGTAAATAATACAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTTCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41	A G	---	TTAGCACATATCTGTGTGGGACTTAAGTGAGACAAGGCAGTAAATAATACAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTTCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38	G T	---	TTAGCACATATCTGTGTGGGACTTAAGTGAGACAAGGCAGTAAATAATACAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTTCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62	T C	---	ATTACAAATCCTACCTAGCACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGATC/G CTGCCAGACCAATAAGCTTTCTTTCAAAACAATTTGTAAACCTCCTCCTTCCTTAATAAACCTAAG ATTTCTTTGTTCCCTGACATCTGAAGGCCACGCTGTCTAGATGTATGTCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAAGAAACCTTTTACTTAGGGATTGTCT
WI-2971	62	T C	---	ATTACAAATCCTACCTAGCACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGATC/G CTGCCAGACCAATAAGCTTTCTTTCAAAACAATTTGTAAACCTCCTCCTTCCTTAATAAACCTAAG ATTTCTTTGTTCCCTGACATCTGAAGGCCACGCTGTCTAGATGTATGTCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAAGAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGGTGCJTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151	G C	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGGTGCJTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133	A T	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGGTGCJTAAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT

WI-3292b	106	GA	---			<p>GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTGCACTATCC TCCCTGCCCCGTCAGCCCTATGTTACTGGTATGCTGATGGTATGGATGGGATGATTACTT GCCATGAATATTTCCATTGTTCTCATTAATGTTAATTAAGTAAATATATTATTTNCCATGA GACACAATGGAAATGGAAACATTCATGGAAAAAACCCATTCAATC</p>
WI-3292	106	GA	---	---		<p>GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTAGCTGCACTATCC TCCCTGCCCCGTCAGCCCTATGTTACTGGTATGCTGATGGTATGGATGGGATGATTACTT GCCATGAATATTTCCATTGTTCTCATTAATGTTAATTAAGTAAATATATTATTTNCCATGA GACACAATGGAAATGGAAACATTCATGGAAAAAACCCATTCAATC</p>
WI-3355	19	GC	---	---		<p>CCATGAACCATGGCTACA/GC/ATATTCCTAACTTCAGAGTCCCTCTTACTGGAGGGATCCA CTTTTAAATATGATTTCTGAAGTGGCTGCATCTATTCCTCCAGCACTTAAACTCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATCTTTTGGATCAGTTTAGATGACTTTNAGTTG</p>
WI-3408	194	GA	---	---		<p>CCATGAAGAAATGAGTTCCCTCCCTGGGTACGCTAAGAATAGCACCCCTTGAGAAATTTNACT TAGCAGTGGCATTTGTAATGGCTGGATTTCCTCCGCTTAAGACACACACCTTTATGCTTTNAGCTTT CTGGAAATGGGATGAATCTNACATTCATGTCACCCCTCGTGTGGGATCCTCTCQ/GA/JGCCCC ATCTCTGNAGAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG</p>
WI-3505b	131	GA	---	---		<p>TAACCTATGCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCTCAGTGCACCTTAAAAATATTTT GAAAAATGGCATTTTAAATATCTTTGGAACCTCTTAACACATTAACCTATTTTNAACCAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT</p>
WI-3505	131	GA	---	---		<p>TAACCTATGCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCTCAGTGCACCTTAAAAATATTTT GAAAAATGGCATTTTAAATATCTTTGGAACCTCTTAACACATTAACCTATTTTNAACCAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT</p>
WI-3564b	177	CT	---	---		<p>GCTAGTAGGTTCCACCTAAATGGTTCCAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTCTCCAGGTATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTACGTTAACATGCATGCTGTTCTTACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCCCTTCACAAAAACAAA</p>
WI-3564	177	CT	---	---		<p>GCTAGTAGGTTCCACCTAAATGGTTCCAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTCTCCAGGTATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTACGTTAACATGCATGCTGTTCTTACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCCCTTCACAAAAACAAA</p>

[illegible]

WI-4230	93 T	---	---	AGAGACGTGTAATGGGACATCTTTCTATTTCGATTAGTTTAAAGATTGATGAAA GTTTGCACATCCAGATTATCTTTATAGCAGCAGAAAGCTGGCAATTAATACACACACGTGACT TTTCCATGGTAAAGAGAGATTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTTAAATGGAGGAGATGATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 C	---	---	GAAATCCATTGAAGTTTGACCTTGAACCTGATCTCATTAATCTTTTCTAGTGGTTGATTT CATTTTGGACAACAGACAGACGAAAAATTTCCACTTAAATTAATCTCTCTAAGTATCTATGAT TTAGCACTGTAGCACCAAGCTGTGAAATTAATCTCTAGATATCTTCAGAACTAGGATGGAAG AA
WI-4271b	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGATNCTACAGGAGCCCCAACCCCTTTGTCACAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGATNCTACAGGAGCCCCAACCCCTTTGTCACAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G	---	---	AATCGAACCATTTGATTTTGTGTAAGGAACACATTTATGATATTTTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/GA/ATNGCAAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 G	---	---	AATCGAACCATTTGATTTTGTGTAAGGAACACATTTATGATATTTTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/GA/ATNGCAAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A	---	---	GATGACAATTATTGTGATTGGCATTTTAA/G/ATGACCATTCCATTTCTCTGGCTTTGGTGTGT TGTTGTTGAGAAAGTCAGGGGTAGTGTGTTTCTCTCTCTTTCTAGTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAAATCAAAATTG TATTCTCTATGCTTAAATGCTCAG
WI-4491	145 GC	---	---	ACCATCAATGATACCTCTTAAATTTATTAGATGATTAACCTGGCTCTGTTAAAAATAAAAAACCT GTCTTGGACATTTGAAATAAAACATTAATTTGGTCAATTTTCTGCTACTTACAAAGGTACTGCACTA AACAAAGTTAAG/GC/GTGTTTTGGAGGGGAAATCATAAAAATGCATAAAAAATTTCTACCACGTGCA TTTCTGTGCCATAATAAAATTTTACATGCT

WI-4584	144 A G	---	TTGGTTGGCATTAGCCCTATACAACTATTACAATCATATTGTTACTCTATTATTTACAAACAAG AAAAATGAGGCTTAACATCACACTCTGCTTAGTCGAGAGCCAGATTTGAACCCAGGAATCCATT CACCGGTAC/AGTGTCTACCTGGTAAATAATGTTAAATTAATCTATGGCAATTAGATTTCAAAGA GTCTAATGTGGTTTGAATAAGGTGGCTTTAAATTTTATCAGTATGC
WI-4639	185 C T	---	TTCTGCATTGAATGTGATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTTTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTTCCAAITCCACCAITTTAC TGACCATATGACTTGGGGAACAATATCTCACCTATCTGAGCTGTATCCGCTCATCTTTAAATTTGTA AATTTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63 A	---	AAATGAATCCGCTTTAGACAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGTGAGAGAG/W- JGATTACTCATAAAAGCATATTAATTTTATAAATATGGAATAATTAACATAGATAAATTAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTCGGATGACAAATGATGAATGTTCTAAGCAGACAG
WI-5390	87 C T	---	GCCTTTGAGAAATGAAGGGGAGCTGGACCATTCGAGGGCTCTTCATCTCTGATTTTGTGTAT TTATTGTTCACTTATTATTC/CTGCTCTCCCTCTGGTATGCTTGTGTCATGAACAATGAATTC CCAGTGGCTGGCCCGAATTCGGCTCTAGAGGTGCCAGAAAAAGTTTCGGTGAATAGAAATG ACGAATGGGTTCAGAAATGAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A	---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAGAAATCAATTAATTAAGCAGT GCAACATTTATTTAATTTT/AAATTTT/AAAGAAACCTGTTTCTGAACTTTGTACTCTTTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTGTGATCCACCCCATCTCTTTTCCACAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5404	87 G A	---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAGAAATCAATTAATTAAGCAGT GCAACATTTATTTAATTTT/AAATTTT/AAAGAAACCTGTTTCTGAACTTTGTACTCTTTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTGTGATCCACCCCATCTCTTTTCCACAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5545b	77 A C	---	TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTCCACTCACACTGCCGCCA TATCTCTC/AC/CCCAACACCTCTGTTTCTGACAGCAAGTTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA
WI-5545	77 A C	---	TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTCCACTCACACTGCCGCCA TATCTCTC/AC/CCCAACACCTCTGTTTCTGACAGCAAGTTTCCATCAGTTGATATGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA

WI-5860b	134	A G	ACTCAAGTTGGGGATAAATCAGAAGTTCTATGTACAACCTAAATTTTGTAAAGATTTTATTGT TTCCTTTTATATAAATTATGGATTTGTTTACCTCCCTAACCAACCTTCTAAGGAACTACAC GTTTACTGGAATCATGTGAAGACATTCCTAAAGGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTCCTCAATCATCAACTCTGTAT
WI-5860	134	A G	ACTCAAGTTGGGGATAAATCAGAAGTTCTATGTACAACCTAAATTTTGTAAAGATTTTATTGT TTCCTTTTATATAAATTATGGATTTGTTTACCTCCCTAACCAACCTTCTAAGGAACTACAC GTTTACTGGAATCATGTGAAGACATTCCTAAAGGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTCCTCAATCATCAACTCTGTAT
WI-6106	208	C G	GCAACAACCTATTACTGATTCCAAACCCAGGTCTACTAACCATTAATCAACCTAACCCACAATAC TATATATGTCCTGTTCTGAAATTTTTCATTTAGAACTGTAGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGTCCAGGAGTCTCAATGTGAAGTAAATCTTACAGAG TAAATTCGATAGTAGGTCAACCAAGTCTATTTGTATGAAGGAAAG
WI-6109d	129	T C	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTGAGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAACCTAA AACCTATATTNCTGT/CJCTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG GNAAAATATCCCTGAAATTTTATACCA
WI-6109c	147	T C	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTGAGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAACCTAA ACCCTATATTNCTGT/CJCTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG TGNAAAATATCCCTGAAATTTTATACCA
WI-6109b	147	T C	AAGATAGACAAACATATGCCAGACCAACAAACACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTGAGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAACCTAA AACCTATATTNCTGT/CJCTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG GNAAAATATCCCTGAAATTTTATACCA
WI-6109a	129	T C	AATGCTATCACCTTCATCATGTCATACGATTGATTCAATATGCTTATTGTTAGCACCTGTC TTCACACACATGCTGTTGTTCAATGAT/CJGCATATCCCAAGTGCCTTAGACAATGCTCCCATAC AGTGAACAGTATTGACTAAACACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6112	96	T C	

WI-6244	103	T C	TAA TTGCACAAC TTACATATCAGGGTTCTGATTGAAAGGAAGAGAAATATTCCTTTCTTTAGTGATT GCTTAATATTAATTCATAATAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACGAGGAGACATTTTATATACCTACAGTGGGGAAGACTT CCTATTTCTTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	C T	CTGGCCTTATAATCCAAAGTTTAGGATTAATCTTACCCCACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTCTCTCCTAGTAGGCTTTGGGTGTGGCACCCTTTGGCTCATTC/CTACTCTCCCT GGGTCTATTGACTTTTACAGGAGCCCTAGAAAGAGCTGGACAAAACCTGCTTTTTCAGAAAAGAGTCG GGGTCCAAAGATTCTGTTACGATTTTATA
WI-6336b	234	C T	AGGTGCCATTATCCCATCAAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATTCCTCCCTTTTACATGTTTCTTATAGACATACAGTTTAACTCAATTAACAACCTAAACAGCTT ATATCTGGCAATATATACAGATGGGTTTATGTCAGAGTAAATAGATCAGATGAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCC/CTTGGAGACACTGACAGT
WI-6336	234	C T	AGGTGCCATTATCCCATCAAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATTCCTCCCTTTTACATGTTTCTTATAGACATACAGTTTAACTCAATTAACAACCTAAACAGCTT ATATCTGGCAATATATACAGATGGGTTTATGTCAGAGTAAATAGATCAGATGAATGGACCATGTG GTACCCAGTGCATTATGCTTGGTAGAGCC/CTTGGAGACACTGACAGT
WI-6381	92	C A	TTGGATACAAAATTCAGTTACACAAATCAGTAGCATTCAAATAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTAAACA/C/AGTATTTTAAAGCTCAAACATTTTAAACAGGCACAAT ATTCTAANGCATATGCATTCACCTGGGCTTTGAATGTCTCCTCACTCCCACTCAACATCAAATC TACAGANGCGGCAAAAGATCAGAGTTTCA
WI-6436	198	C G	GGTTGAGGCATTGGGAAGGCGAATTTGAGGCGAGTGAATAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCAATCAGACAGAGAAATACAAGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTTGGTGTCATAATAAGAAGTTAGACTTTGGTGTGTAGTAGTTGTAGTAGGTAGGTAGCGTT/C GATGGGTGATTTCCACAGACAAGGTGATGTTCTAAGATTGATATTTATTTG
WI-6449	186	C T	GAGGCCTCTTTGCTTTCTCCTCAGTCAAGGCTGATCCAGGTTGATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTGAAATC GTATCTGGTTCTATTCATCTGCTGATCTTATGCTGGCTCTATTC/CTATCCCTATTTCTCTGA TCTATGTGACAGCTGAAGTTCCCTCTAATTTTCTGTGGTGTATTTATA
WI-6449	186	C T	GAGGCCTCTTTGCTTTCTCCTCAGTCAAGGCTGATCCAGGTTGATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTGAAATC GTATCTGGTTCTATTCATCTGCTGATCTTATGCTGGCTCTATTC/CTATCCCTATTTCTCTGA TCTATGTGACAGCTGAAGTTCCCTCTAATTTTCTGTGGTGTATTTATA

WI-6463	72 T C	...	GCTGGAGAGAAAGACCTCCAAAGAGAAAGAACTAAATCAGAGTCTTTGAGCAAGAGAAATTGAAA AGAACA(T/C)TGAAAAAAATTAAGTAGAAGTCAAGAGCCAAAGTCCCAATTGTGTCATTAA TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATGATCAGTTAAATGTTCTCTCTCTC CAGTCCCATTTATATGACATTCGGCATGCTG
WI-6474b	76 C T	...	AAGCAGTAAATCTTCATCATGCGATGCGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGCAAA(C/T)GTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACITGCTTAGAGCC AAGAAAAAGTAGAATTTGAAAGGCACAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATATAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T	...	AAGCAGTAAATCTTCATCATGCGATGCGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGCAAA(C/T)GTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACITGCTTAGAGCC AAGAAAAAGTAGAATTTGAAAGGCACAGAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATATAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A	...	GAACCTAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTACCTCTCCCAATAGTGGAGAAATCAGAGT(A/G)CTCTTGTCTAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A	...	GAACCTAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTGAGATT TTGGACCTTGGTATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTACCTCTCCCAATAGTGGAGAAATCAGAGT(A/G)CTCTTGTCTAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A	...	CACATTTGAATGCAACTGAGAAANTGGTTTNTAGGCTTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA(G/A)TCAAATTTTAAAAAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTCTTC
WI-6564b	54 G A	...	TTCTTTATTGGTCTTACCAATGTGACTCTTTACCCAGGCCACTGTCTCTATGCG(A/C)ACTGGCTTG TAGGCATTACATCATATGCTGTCTGCTGAAATCTCAATTAATTCCTCNCCTATTCCTTTTCCAT GCTCTGCTCATTTNCTCAGAAATTTGAAGGCAATTGATTATNATTTTTTTTGGTCTGTGTAAAG GTTCTTGGCAGGAGAACATGACATATGACTTTTAAATAAAGACCAACA
WI-6564	54 G A	...	TTCTTTATTGGTCTTACCAATGTGACTCTTTACCCAGGCCACTGTCTCTATGCG(A/C)ACTGGCTTG TAGGCATTACATCATATGCTGTCTGCTGAAATCTCAATTAATTCCTCNCCTATTCCTTTTCCAT GCTCTGCTCATTTNCTCAGAAATTTGAAGGCAATTGATTATNATTTTTTTTGGTCTGTGTAAAG GTTCTTGGCAGGAGAACATGACATATGACTTTTAAATAAAGACCAACA

[illegible]

WI-6710	106 G A	---	---	CCATGACAGTTAATTAGGAAGCTTCGACTTGTTAGAAATAACAGAGGAAGTCCAGTTATCTACCT ATTCTTAAACACATTTTGTGAGGCTGGAATGATTCGCGATAGTAAACTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTATTAGTGAGTCGACAGGATGTCACCGTGAAGGCTC ATCCAGTCCCAATGGAGGAGTTGACTTAGACCTTCCTTGACAGGAAGGCTC
WI-6766b	148 G C	---	---	AAACAAATGGTGCATTGCATAATTTTGGTGCACAGTATAAAACAATAAATAGTTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCCTTATGT GCCACACTTAAAN(GC)AAAGTCAAGTTTCTCTCTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGGNGAAGTTACCCAAATCCAGTTCCCTCTTC
WI-6766	148 G C	---	---	AAACAAATGGTGCATTGCATAATTTTGGTGCACAGTATAAAACAATAAATAGTTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCCTTATGT GCCACACTTAAAN(GC)AAAGTCAAGTTTCTCTCTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGGNGAAGTTACCCAAATCCAGTTCCCTCTTC
WI-6787b	97 A G	---	---	ACAGATAAAGTCTTTATCCCTGTATTTTACATAAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTTCAAAATTTACAGTGTCTTCTGCTACGATAAGATATCTTCATGTACAAGTGT ATGCTTGTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAACACACATCCACATGACAAAGGA GAGTGAATAGGGCAGAGTAGANTACTACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G	---	---	GAACCCACCGGCTCCTGTTATTTTAAAGGAGCATTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGCGGCTCTCAATCAATCAGTCAACCCGCGAGGTAGAAAGTAGAGTCAATGAGGAA GAGCTGTGCTGTAGGAAGTAGGTTAATGCCCTTAATCCCGGAAAGGGGCGAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTCATCAGGTAAAGGCAAC
WI-6810b	37 T C	---	---	CACAATAATAAATCACTCCCTACCTTGAACCTTAT/CJAGAAAGCATTTTTTAAITTTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTTAAAAATGTTATGNACAGTACAATTTCTTTTGTGTTCTGCAGCAATGACC ACTAAGNAATAATTTTAAAGGCTGAACAGAAATCCAGCGCAATGAAGTTAAT
WI-6810	37 T C	---	---	CACAATAATAAATCACTCCCTACCTTGAACCTTAT/CJAGAAAGCATTTTTTAAITTTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCTTTTAAAAATGTTATGNACAGTACAATTTCTTTTGTGTTCTGCAGCAATGACC ACTAAGNAATAATTTTAAAGGCTGAACAGAAATCCAGCGCAATGAAGTTAAT
WI-6817b	145 C A	---	---	GCATGATTAAACGAGTGCAGAAAATACCAAGTACATTGGTGAACGATGAGTGTCTTAGTA TTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAACTATCACTAATCACTAACAATGTAGCT GCAGGGTAAACG/ATGTGGATACCTGTGCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAAATCTTGTTCAGGTGCGGCTGTGTGCAG

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WI-7136	58 T C	---	<p>TGTGAAGCCACATTTTCCACATGAGCCTCATGAAGCCAACTAAGTGTATTATGAACGTGTCTAATTC</p> <p>TCTCAATAACTCAGTGTAGCAGCTTTAAAGTGTGAAGCAGCAACATGAAGAGCATATCAATGTGTG</p> <p>GTGGAGAAAGGGAAGGGTGGCTTTTAAATTTATTTCTCATCTTTTATACAAGAAAGNNNNIN</p> <p>NN</p> <p>TTTCTATATG</p>
WI-7146c	210 A G	---	<p>GGGACGCTGTGTTTGGCTCAATTTGGTGTGTGGTCAATGAGGCTCTCCATTTGCTTTAGCTG</p> <p>AATAATGAGTTGTTCTAGAGGAGACAGCTGTCTCCTTTGTCGCCCAAGCCCATGCCCTGCCG</p> <p>TGGTGGCAGCTGGGCTGTGATGGAGGGGTCCCAACATGATGTTTGGCCCTCTCTGGCATGCC</p> <p>AACGCAGTGTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA</p>
WI-7146b	210 A G	---	<p>GGGACGCTGTGTTTGGCTCAATTTGGTGTGTGGTCAATGAGGCTCTCCATTTGCTTTAGCTG</p> <p>AATAATGAGTTGTTCTAGAGGAGACAGCTGTCTCCTTTGTCGCCCAAGCCCATGCCCTGCCG</p> <p>TGGTGGCAGCTGGGCTGTGATGGAGGGGTCCCAACATGATGTTTGGCCCTCTCTGGCATGCC</p> <p>AACGCAGTGTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA</p>
WI-7146	202 GA	---	<p>GGGACGCTGTGTTTGGCTCAATTTGGTGTGTGGTCAATGAGGCTCTCCATTTGCTTTAGCTG</p> <p>AATAATGAGTTGTTCTAGAGGAGACAGCTGTCTCCTTTGTCGCCCAAGCCCATGCCCTGCCG</p> <p>TGGTGGCAGCTGGGCTGTGATGGAGGGGTCCCAACATGATGTTTGGCCCTCTCTGGCATGGA</p> <p>CCCAAGCAGTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA</p>
WI-7153	161 A T	---	<p>ATATTACAAGTGTCTTTAGCTGATCTCCATCTCAATGAGCTCTTTTCTTTATATGTTAAACATA</p> <p>TATAAAATGGCAACTGATAGTCAATTTTGAATTTTATCAGGAACATCTGAAATCTGCTCAGAGCT</p> <p>ATGTGCATAGATGAACNNNNNNNNIA/TJAAAAAAGTTATTAACAGTAATCTATTACTAAATAT</p> <p>AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAAATGGTATGTTT</p>
WI-7155	156 T G	---	<p>TAGATAGATGGGTCATATCTCTTTGGCTTCTGGTCTCCAGCCCTCATGGTTGGCATCACATAT</p> <p>GCCTGCATGGCCATTAAACAGCTGCCCTACCCCTATAATGATCGTCTGCTCAATTAATATACAC</p> <p>CAGTGGTTCCTCCTCCCTGTGTJTAAGAGACTAATGCTCAGATGCTTTACCGAATTTATATTCTAG</p> <p>CTCAGCTCTCTGTGCCACCCCTCTCTCTCTCCCAATCCCACTCCAG</p>
WI-7159b	161 A G	---	<p>AGCTCCACAGATGCAGATTTGTTGTTTCTTTCTTTATCATCTGTCACACAGCTTATAACATGTAT</p> <p>GCTTTTCAGAAATACAGTTGTCTAGCCCAAGCCATCAAGTGTCTGAAATCTCAATTTGTTTATGCAAT</p> <p>ACAGCAACTTTTATTAAGTAGATAGJGGAGAAATATGTTTAAATATTTAGGAATCTCTAGACCATA</p> <p>TTTCAAGTCACTTAGCAGCTAGGATCTCAAAATGGAAGTGTATATATA</p>
WI-7159	194 C T	---	<p>CTCTAGACTAGTGTCTTACCTTTTAAATGAAGTGTACAGGAAGCCCAAGCAGTGTCTCTCAACCA</p> <p>ATAACTTCAGAGAAAGTGTGTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATACCACTC</p> <p>AGTTCTTGGTTTCAGTTGACAAAATATATATGTTTACTGCTGTCACTGTCCCATGCCATCTATGAT</p> <p>AAATTTATTTTGAATTAATAAAAAACATTTGTACATTTCTGTACTGCGG</p>

WI-7175	194	C T	CTCTAGACTAGTCTTTACCTTTATTATGAAGTGTGACAGGAAGCCCAAGGCGAGTGTCTCTACCA ATACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCTACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTTACTGCTGATGTCCATGCTCTAICTAGAT AATTTATTTTGTATTTTGAATAAAACATTTGTACATTCCTGATCTGGG
WI-7178b	273	G A	TGTATCAGGTGAGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCGAGCTGCGCTGGAG AGGGTCTCGCTGCTACTGGCTGCTCTAGGGGAACAGACCGTGCACCCAGAAAGCATACACCA ATCCAGGCTGGCTCTGCACCTAAGAGAAATTCGACTAAATGAATCTGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273	G A	TGTATCAGGTGAGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCGAGCTGCGCTGGAG AGGGTCTCGCTGCTACTGGCTGCTCTAGGGGAACAGACCGTGCACCCAGAAAGCATACACCA ATCCAGGCTGGCTCTGCACCTAAGAGAAATTCGACTAAATGAATCTGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116	A C	GCATATTTGGCAGCTTATGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACCAAGTTCCTCTGCAACCCAC/ATCTGAGCCCTATCTCTCTCTATTT TACTTGAGGCTGCCAATTACCAAGCCAGCTTTCAGCTCAAGAGATGCTTAAGATAATTATGTGAGG CCACTTGTAGCAAGATGGCAGCTATTTCTGAAAGCCCTAGTACCCCAAT
WI-7182	106	C A	GCATATTTGGCAGCTTATGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACCAAGTTCCTCTGCAACCCAC/ATCTGAGCCCTATCTCTCTCTATTT TACTTGAGGCTGCCAATTACCAAGCCAGCTTTCAGCTCAAGAGATGCTTAAGATAATTATGTGAGG CCACTTGTAGCAAGATGGCAGCTATTTCTGAAAGCCCTAGTACCCCAAT
WI-7191b	273	T A	ATAATTGCTTTTCTAGCTGGCAAGATATTTTCAAAAGAGGGAACAATGCTGATTAATCTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACACACACATCTAAGCATTAAGTATGGTATGAGC TGATTCAGCTTCATGTGGATTTTAAAGCACTCTAGAAACAATGAAGCTTCTTGGCATATTTAAGGAG CTCCCAAAATGTTACCTATTAAATTTGAACCTACGCAAGTAGAAGACCAAT
WI-7199c	112	T C	CCAGTGGTGAACAGAACCTCCCAATTTGAGTTCACCCCTTCCTGTGGCTTATGAGCTCAGCCTC GCTTTGAGGTACCAACCGTCTGTCAGCTCTTTCAGCTTCTGTTGGTCTCTGAATTTCTCTTTATAT TGGGAGTTAAGGAGGAATAGCATTCCTTAATGTTTGTGGTCTCTGAATTTCTCTTTATAT AGTCTATAGTTTACTCTCAGTTCCTCACCATCATCTTGTCTAA
WI-7199b	112	T C	CCAGTGGTGAACAGAACCTCCCAATTTGAGTTCACCCCTTCCTGTGGCTTATGAGCTCAGCCTC GCTTTGAGGTACCAACCGTCTGTCAGCTCTTTCAGCTTCTGTTGGTCTCTGAATTTCTCTTTATAT TGGGAGTTAAGGAGGAATAGCATTCCTTAATGTTTGTGGTCTCTGAATTTCTCTTTATAT AGTCTATAGTTTACTCTCAGTTCCTCACCATCATCTTGTCTAA

WI-7216c	237 T C ...			TGACACTAACACTCTAAATCAAGCGAATGTTGGAAACACCATGACCTCCTGTGTGTGTCCTTTCTCCCG AAGGACAAAATGTAGAAAAGATGTAGATAACTTACTCAAGATCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTTTTCCTGTGTATCACTT
WI-7216b	237 T C ...			TGACACTAACACTCTAAATCAAGCGAATGTTGGAAACACCATGACCTCCTGTGTGTGTCCTTTCTCCCG AAGGACAAAATGTAGAAAAGATGTAGATAACTTACTCAAGATCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTTTTCCTGTGTATCACTT
WI-7220b	147 A T ...			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTTGTCTTTTAAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGATAAAGTAGACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTT
WI-7220	140 A T ...			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTTGTCTTTTAAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGATAAAGTAGACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTTAGTGTGTT
WI-7226	232 C ...			GATCGAATTTTCAGATGATCGGAAATTTTCAGGTATTTGTAAATAGTGACATATATATGTATA TACATATCACTCCTCTATTTCTTAAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCAT CCCTTTCCATATAGGAACATAATTTTGAAGTGGCCAGATGAGTTTATCATGTCAAGTGAATAA TTACCCCAAAATGCCACCACTTAACGATCTTCACTTCTTGGGGTTT
WI-7228b	254 G A ...			ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACAGTAATTTGGCTCCAAATTCATAA TATGTTCCACAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAACTTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGATCAGAGATATCTTTTGTGCTAGATTGCAAAATCTCCAAATCCACA CATATTGTTTAAATAAGAAATGTTATCCAACTATTAAGATATCTCAATGTT
WI-7228a	163 G A ...			ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACAGTAATTTGGCTCCAAATTCATAA TATGTTCCACAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAACTTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGATCAGAGATATCTTTTGTGCTAGATTGCAAAATCTCCAAATCCACA ACACATATGTTTAAATAAGAAATGTTATCCAACTATTAAGATATCTCAATGTT
WI-7233c	213 C T ...			CGATCGTACTGCCAGTAGCATTTGTCTGTCTCGGCTTGTGTTGTACATTTCCATTTCAATTTGTACA GATGTGAACCTTATCTCTGTCACTAAATATATTTAAAAATTTTCTAGGAAGTCAAAAATATAA TAAAGGGTTGAGCCCTTACTTCTCTTGCACCTTTTGTGGCAATTTAAAGTGAAGTGAATGCTAATA GTGTAAGTATCTGTGTGCACAAAACCCACTGCCAGATAACGAGGGGCGCTG

WI-7233b	213 C T	...	CGATCGTACTGCCAGTAGCATGTCTGTCTGCGGGTCTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTGTCACTAATTTATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCCACCTTTTGGCAATATTAAAGTGAAGTCTCTAATA GTGTAAGTATC/TGTGCAAAACCACTGCCAGATAACAGAGGGGCGTG
WI-7233	211 T C	...	CGATCGTACTGCCAGTAGCATGTCTGTCTGCGGGTCTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTGTCACTAATTTATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCCACCTTTTGGCAATATTAAAGTGAAGTCTCTAATA GTGTAAGTATC/TGTGCAAAACCACTGCCAGATAACAGAGGGGCGTG
WI-7238	128 T C	...	GCGTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACATTTTGTCTTAGTCTTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTGTTTCTGCGTT CTGTTTAAACAGAAATAAAGAGGTGTAAGCTCTTTTCTCATTTCAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAAACATTCAAGTAGAATTTTATGCTTA
WI-7252f	520 T C	...	CCACAGGATCCAGCCAGCCAGGCGCCCTCCCGCCCTTCCACTGCGACGACGCGCGGGACAGAG GCCTGCGCGGGCGCCAGCCCGCCCTGGGCTCGAGGCTGCGGCTTCCCA
WI-7252e	552 T C	...	CCACAGGATCCAGCCAGCCAGGCGCCCTCCCGCCCTTCCACTGCGACGACGCGCGGGACAGAG GCCTGCGCGGGCGCCAGCCCGCCCTGGGCTCGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTTCCCA GACACTCTCTAGAGAACGCGCCCTAGAGGCTGCTGCGAGGCTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTCTGAGGATGTCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252d	540 T C	...	CCACAGGATCCAGCCAGCCAGGCGCCCTCCCGCCCTTCCACTGCGACGACGCGCGGGACAGAG GCCTGCGCGGGCGCCAGCCCGCCCTGGGCTCGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTTCCCA GACACTCTCTAGAGAACGCGCCCTAGAGGCTGCTGCGAGGCTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTCTGAGGATGTCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252c	552 T C	...	CCACAGGATCCAGCCAGCCAGGCGCCCTCCCGCCCTTCCACTGCGACGACGCGCGGGACAGAG GCCTGCGCGGGCGCCAGCCCGCCCTGGGCTCGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTTCCCA GACACTCTCTAGAGAACGCGCCCTAGAGGCTGCTGCGAGGCTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTCTGAGGATGTCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA
WI-7252b	540 T C	...	CTCCTCTCTCTGAGGATGTCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCA

WI-7252a	520 T C	...	CCACAGGATCCAGCCCAAGCGGCCCTCCGCGCCCTCCACTCGACGACGACGCGCGGGGACAGAG GCGTGCOCGGCGCGCCAGCCGCGCCCTGGGCTGGAGGGTGGGCGGCGGCGGCGGCGGCTGCTGCTGCTGCGG GACACTCTAGAGACGCGCCCTAGAGCGCTGCGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252 T A	...	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265l	231 T A	...	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G	...	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A	...	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C	...	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A	...	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTATTTGTTTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G	...	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCCATCTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGTATTTGTTTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231	T A	---	---	AACTGGTTATGTCAGTTCCTGCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTCACCCATTCTGTGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGATAGTATTTTGTATATATATGTAATAATAACGATCTCT AAAAATACCACAGTTGTATTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7265e	227	T C	---	---	AACTGGTTATGTCAGTTCCTGCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTCACCCATTCTGTGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGATAGTATTTTGTATATATATGTAATAATAACGATCTCT AAAAATACCACAGTTGTATTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7265d	174	T A	---	---	AACTGGTTATGTCAGTTCCTGCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTCACCCATTCTGTGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGATAGTATTTTGTATATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTGTATTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7265c	170	T G	---	---	AACTGGTTATGTCAGTTCCTGCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTCACCCATTCTGTGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGATAGTATTTTGTATATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTGTATTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7265b	121	T G	---	---	AACTGGTTATGTCAGTTCCTGCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTCACCCATTCTGTGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGATAGTATTTTGTATATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTGTATTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7265a	80	T A	---	---	AACTGGTTATGTCAGTTCCTGCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTATTTGCCACCAAAAGTAATGCAATTTTCACCCATTCTGTGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGATAGTATTTTGTATATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTGTATTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7281b	183	C	---	---	GATCAACCCAGCCACCAAGCCCTCGAGGCCCTATACCATGGCCCACTTGGAGCAGAGGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCCAAGTCTGCCAGCCTGCCCTGCAGGTCTCCATGAAGGCA CCCCATGGTCTGATGGGATGAAGCATCTCAGACTCTCAGACTCTCAGTCTGCAAGAGGCCCTCTC GTGTGTGAAGACCACTGCTCTGTGTGGGTCTGCAAGAGGCCCTCTC
WI-7281	171	C A	---	---	GATCAACCCAGCCACCAAGCCCTCGAGGCCCTATACCATGGCCCACTTGGAGCAGAGGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCCAAGTCTGCCAGCCTGCCCTGCAGGTCTCCATGAAGGCA CCCCATGGTCTGATGGGATGAAGCATCTCAGACTCTCAGACTCTCAGTCTGCAAGAGGCCCTCTC CAGGTGTGTGAAGACCACTGCTCTGTGTGGGTCTGCAAGAGGCCCTCTC

WI-7301	205 A C	---	---	ACTATGGCAGTGGTCTGGTTATAGTAGTAGAGCGGGATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATATGATTTTGGAAATTCAGATGGAGCAACAGCAATCA AATTACGTGGACACATGAAGGGGCGAGTTTGGTGGAGAAAGCTCGGGCAG
WI-7314c	49 GA	---	---	CTCTCTTTTCTTCAGATCTGCTCGGTTTAAITTTGGGAGGTCA/GA/TTGGTGTCTACCTCACTG AGAGGAACAGAGGATATGCTCTCTTTGCAGCAGTGAATAAGTCAATTAAGAACTCCACAG ATTCTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATATGAACGCTCTTCTCCAGGA CAGAAAATGTGTAGTGTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314b	49 GA	---	---	CTCTCTTTTCTTCAGATCTGCTCGGTTTAAITTTGGGAGGTCA/GA/TTGGTGTCTACCTCACTG AGAGGAACAGAGGATATGCTCTCTTTGCAGCAGTGAATAAGTCAATTAAGAACTCCACAG ATTCTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATATGAACGCTCTTCTCCAGGA CAGAAAATGTGTAGTGTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7314	36 A G	---	---	CTCTCTTTTCTTCAGATCTGCTCGGTTTAAITTTGGGAGGTCA/GA/TTGGTGTCTACCTCACTG AGAGGAACAGAGGATATGCTCTCTTTGCAGCAGTGAATAAGTCAATTAAGAACTCCACAG ATTCTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATATGAACGCTCTTCTCCAGGA CAGAAAATGTGTAGTGTACCTTTATTTTATTAAACAAACTTGTTTTT
WI-7321b	199 C T	---	---	ACTCAGGGAAGGGATGCCCATTAAGTGCACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCTGCACAGTCAAGGAGCTGCTTTGGCATCCAGGCGCTCCA GTCACTCACTGCCATACATTAGAAAATGAGACAAATCAAGNNNNNNNNAGGTGGCACACCCATC/C /TGTGTCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGCTGGCCA
WI-7321	199 C T	---	---	ACTCAGGGAAGGGATGCCCATTAAGTGCACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCTGCACAGTCAAGGAGCTGCTTTGGCATCCAGGCGCTCCA GTCACTCACTGCCATACATTAGAAAATGAGACAAATCAAGNNNNNNNNAGGTGGCACACCCATC/C /TGTGTCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGCTGGCCA
WI-7336b	248 A C	---	---	AGACATTCGCTTCCTGAAAGACTGAAGAAGTGTAGTCATGGGACCCAGGAAACTGCCCTGGC TCCAGTGAACCTTGGGCACATGCTCAGGCTACTATAGGTGCAAGAATATGGCAAAAGGCTTACCTTGGCAG GCAGGTGTTTATTAATTTCTGAATTTGGGATTTCAAGAATAATTTTACATACACTGTATGTAT TATAGAATTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA/CICA
WI-7336c	221 A G	---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAACCCAGGCTACATGCCAATGATAGGTGCAAGAATATGGCAAAAGGCTTACCTTGGCAG CAITATTTGTGTGACAGAACAAAGAACAGAAATCAATATATAAATTAAGAAATCTGCAGCTA GTGTGTTCTCTTTACACAC/AGT/TATACACAGACATCAAGAAATCTGTGT

WI-7338b	125 A C	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTCTTTTJWJCCTTG AGCCATTATTTGTGCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATCTGTT
WI-7338	125 A C	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTCTTTTJWJCCTTG AGCCATTATTTGTGCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATCTGTT
WI-7338	221 A G	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTCTTTTJWJCCTTG AGCCATTATTTGTGCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATCTGTT
WI-7384c	146 T A	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTCTTTTJWJCCTTG AGCCATTATTTGTGCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATCTGTT
WI-7384b	146 T A	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTCTTTTJWJCCTTG AGCCATTATTTGTGCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATCTGTT
WI-7384	145 T A	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTCTTTTJWJCCTTG AGCCATTATTTGTGCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATCTGTT
WI-7388c	106 A T	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTCTTTTJWJCCTTG AGCCATTATTTGTGCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATCTGTT
WI-7388b	106 A T	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTCTTTTJWJCCTTG AGCCATTATTTGTGCAGAGAACAAAGAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTTTACACACATATACACAGACATCAGAAAAATCTGTT

WI-7388	94	T A	TGAAATCCTGGGTCTCTGGCTGTCTGTAGCTGGTTATTTTACTTTGCCCCCTCCACATTTTT TGAGATCCATCCTTTATCAAGAAATGCTGAAGCGACTATAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGTTTACCTCTATTTTGCCACAAGCGTCTCGGATTTGTTTGA CTGTGCTGTGCAAGAACTTTTCCCCCAAGATGTATAGTTATGG
WI-7438	64	A G	TTAGATTTTAATTGGCAACCACTCACTGCCACCATCCACTGCAGATCTNCTATTCCTGGGAGJ GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTCAAGTTGNCATGTGCGACAGAGCTCCT TGCTGTAGGTGTAGTCATGTACACTGTACTGTTCACGTGTACATAGTTTGTGNCCTGGTATTTGTTA TTGGAATGAATATCGCTTCCACTGACITTTACCA
WI-7454b	152	T C	CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCTGTGGTGTACCAACAAAGCCCAACCC CAGTACAACTGAGATGAGAGAACCTGTAGCACTGTCTGAATGCCAGGAGCTTCCAAGGCTAA TCCTACCCCTGGATTCTTTCGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCATTGTCTACTTCTCAATGTTTTGACA
WI-7454	152	T C	CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCTGTGGTGTACCAACAAAGCCCAACCC CAGTACAACTGAGATGAGAGAACCTGTAGCACTGTCTGAATGCCAGGAGCTTCCAAGGCTAA TCCTACCCCTGGATTCTTTCGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCATTGTCTACTTCTCAATGTTTTGACA
WI-7464c	177	G C	AATTTGAAATCTGAAAAAAGTGCAATAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACCTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTTTCTATGTA CAACAGAGCCACAGCACAAGGGTGGGCATAGCAGTTGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAACGTTACCAACAATAT
WI-7464b	168	C A	AATTTGAAATCTGAAAAAAGTGCAATAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACCTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTTTCTATGTA CAACAGAGCCACAGCACAAGGGTGGGCATAGCAGTTGCCAGAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAACGTTACCAACAATAT
WI-7464a	103	C A	AATTTGAAATCTGAAAAAAGTGCAATAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACCTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTTTCTATGTA CAACAGAGCCACAGCACAAGGGTGGGCATAGCAGTTGCCAGAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGAACGTTACCAACAATAT
WI-7499b	134	T G	CAATTTCAATCCAACTAGTGTGTCCTAAACCTTCCAGACAACTTCCACTTCGAAGGTTTAA AATGCATAAGTCAGATAGCAATCCTTCACTTTCCTCCAGAGGACATACGTTCTTTGAATGCTTCAIT /GJTATAGTCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTATAGGA ACTCTGTACAAAATTCCTTTGAAAAATATAAATTTTGGAAATGAGTGATGA

WI-7576b	168 A T	---	---	AATGATGATGATAATGATGATGACGACGACAAACGATGATGCTTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAAATTTTGAAGAGGCGGTAGTGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAACATGGCATCTGCACACAAAAA(A)TGTGGAAGGCTTATCTACATTTTCACTTCACTAC TTTGTAAAGTGAGAGAGACGAAGAAGCAAAANNINNNINNAAGAAAAAATAAAC
WI-7577q	77 T C	---	---	AACCATGTTCCCTCTCTTAGCACCAACAATAATCAAAACCCCAACATAA(G)GTGTGCTTTCCTTTAA AAATATGCATC(A)CAAAATCGTCTCTCATTTCTTCTGAGGGTTTAGTAACACAGTAGGAGTTAAAT AAAGAAAGTTCATTTTGGTTTACAGTAGGAAGAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTAATATGGCCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577p	50 G C	---	---	AACCATGTTCCCTCTCTTAGCACCAACAATAATCAAAACCCCAACATAA(G)GTGTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAAT AAAGAAGTTTCATTTTGGTTTACAGTAGGAAGAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTAATATGGCCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577o	157 G A	---	---	AACCATGTTCCCTCTCTTAGCACCAACAATAATCAAAACCCCAACATAA(G)GTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAAT AGAAAGTTTCATTTTGGTTTACAGTAGGAAGAGAGAGATCAAAAGTGGAGATATGTTAACT ATTGTAATATGGCCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577n	48 A G	---	---	AACCATGTTCCCTCTCTTAGCACCAACAATAATCAAAACCCCAACATAA(G)GTGTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAAT AAAGAAAGTTCATTTTGGTTTACAGTAGGAAGAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTAATATGGCCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577m	84 G A	---	---	AACCATGTTCCCTCTCTTAGCACCAACAATAATCAAAACCCCAACATAA(G)GTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAAT AAAGAAGTTTCATTTTGGTTTACAGTAGGAAGAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTAATATGGCCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577l	93 T C	---	---	AACCATGTTCCCTCTCTTAGCACCAACAATAATCAAAACCCCAACATAA(G)GTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAAT AAAGAAGTTTCATTTTGGTTTACAGTAGGAAGAGAGAGATCAAAAGTGGAGATATGTTAACTAT TGTAATATGGCCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC
WI-7577k	154 C A	---	---	AACCATGTTCCCTCTCTTAGCACCAACAATAATCAAAACCCCAACATAA(G)GTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAAT AGAAAGTTTCATTTTGGTTTACAGTAGGAAGAGAGAGATCAAAAGTGGAGATATGTTAACT ATTGTAATATGGCCCTGTTATACATGACACTCTCTGAAATGACTGTATTTC

WI-7577j	117 A/G	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAGTA/GIACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTATACATGACACTCTCTGAAITGACTGATTTC
WI-7577i	77 T/C	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTATACATGACACTCTCTGAAITGACTGATTTC
WI-7577h	50 G/C	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTATACATGACACTCTCTGAAITGACTGATTTC
WI-7577g	157 G/A	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTATACATGACACTCTCTGAAITGACTGATTTC
WI-7577f	48 A/G	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTATACATGACACTCTCTGAAITGACTGATTTC
WI-7577e	84 G/A	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTATACATGACACTCTCTGAAITGACTGATTTC
WI-7577d	93 T/C	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTATACATGACACTCTCTGAAITGACTGATTTC
WI-7577c	154 C/A	AACCATGTTCCCTTCTCTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCATTTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTAATAATGTGGCCTGTATACATGACACTCTCTGAAITGACTGATTTC

WI-7577b	117 A G	AACCATGTTCCCTTC TCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCTACTTTTCTCTGAGGGTTTGTAGTAAAGACAGTAGGAGTTAAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGACATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACCTCTCTGAAATTGACTGTATTC
WI-7577	107 G A	AACCATGTTCCCTTC TCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCTACTTTTCTCTGAGTAAAGTGTAGTAAAGACAGTAGGAGTTAAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGACATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACCTCTCTGAAATTGACTGTATTC
WI-7619q	106 C G	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTCTAAATTACATGG ATGGCAGGAAGTGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619p	150 T C	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTCTAAATTACATGG CAGGAAGAAATGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619o	228 A G	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTCTAAATTACATGG CAGGAAGAAATGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619n	237 G C	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTCTAAATTACATGG CAGGAAGAAATGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619m	99 C T	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTCTAAATTACATGG TGGCAGGAAGAAATGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619l	189 T A	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTCTAAATTACATGG CAGGAAGAAATGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619k	90 C	---	---	ACAGGGGACTTGAAGAGGACGACGGCTTCAGAGGACAAACCCCAATACAGGAGGACAAAGAC AGAGAGGGCCCAATGGGGTCATCCGCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGCCCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCT CTCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619j	206 T G	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCAGAGGACAAACCCCAATACAGGAGGACAAAGAC AGAGAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCT CAGGAAGATGGGCCCTTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT CGCTTGTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619i	106 C G	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCAGAGGACAAACCCCAATACAGGAGGACAAAGAC AGAGAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCT CTCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619h	150 T C	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCAGAGGACAAACCCCAATACAGGAGGACAAAGAC AGAGAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC CAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619g	228 A G	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCAGAGGACAAACCCCAATACAGGAGGACAAAGAC AGAGAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC CAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT CGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619f	237 G C	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCAGAGGACAAACCCCAATACAGGAGGACAAAGAC AGAGAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC CAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT CGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619e	99 C T	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCAGAGGACAAACCCCAATACAGGAGGACAAAGAC AGAGAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC TGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCT TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619d	189 T A	---	---	ACAAGGCGACTTGAAGAGGACGACGGCTTCAGAGGACAAACCCCAATACAGGAGGACAAAGAC AGAGAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC CAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTCTTCTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619c	90 C G	ACAAGGGGAC TTGAAGGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAGGGCCCAATGGGTCAATCQCGTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGCCCTTAAGGGGAGTGTGGGGTGCTGCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G	ACAAGGGGAC TTGAAGGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAGGGCCCAATGGGTCAATCQCGTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGGAGTGTGGGGTGCTGCTCCCTTTTTCATCTTTTCCCTCTCT CGCT/GTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A	ACAAGGGGAC TTGAAGGAGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAGGGCCCAATGGGTCAATCQCGTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGGAGTGTGGGGTGCTGCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTTTAAACCAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCJAGJTAAACACATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCAAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGCTATTATAGTAAACCAATTTTCTTTGGACTGTTCA
WI-7626c	155 C T	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTTTAAACCAAAAGCAACAGTAA TAATCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTG TACTAATGATGAGCAATTTAGCTTAACTTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGCTATTATAGTAAACCAATTTTCTTTGGACTGTTCA
WI-7626b	28 T A	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTTTAAACCAAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAATGTG TACTAATGATGAGCAATTTAGCAAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGCTATTATAGTAAACCAATTTTCTTTGGACTGTTCA
WI-7626	144 T C	TCCCATAACCGCTGATCTCAGGCTCTCTGCTGCCGCCACCCAGATGGGGGAAAGCAGAGTGGGC TCCCAGTGGCTGCTGCCAGCCGACGACCTTCTAGGACGCCACCCAGCAAGGTTGTTCTTAA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTTGACACTGTGTAAAGAGAGCCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689c	134 A G	

WI-7689b	134 A G	TCCCATAACCGGTGATTCACGGTCTCTGCTGCGGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTGTTCCTAAAJA /GJTAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCGACAGCTGTGTAAAGAGAGCTTAAT GATAATATTGTGTGGTGGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A	TCCATAACCGGTGATTCACGGTCTCTGCTGCGGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTGTTCCTAA AATAAGGGCAGAGTCACACTGGGCAGCTGATACAAATTCGACAGCTGTGTAAAGAGAGCTTAAT GATAATATTGTGTGGTGGCCACAAATAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A	TGGGAACATTCAATCTTGGCGTCACATTTTCATCAATGAAGATTAG/ACACTGAGATCCAGAGAGG CTGGATGACTTGTCTCAAGTTCACCCAGCATGGTAGTGCGAAAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGGGCCACCCAGGAAGCAC AGGTCCAAGGCTGTGCCACACTTATCAGCAGCAACAACCTGTCAGTTCATCC
WI-7703b	164 T C	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTTCACATGGAAACAAGTCAGTCAATCAGATATGATCAAA TGCTATAAACCAAACTGATGAAGTAAAT/CJGGTCTCTCACCTGTTTATTAACTCTAAATTTCT TTCATTTTAGGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156 T C	TTAAATGAGTGTGTTGTCAOCTGGGATTGGGAAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCAGCACTAAAGCAGTGGAC/CACAGGAGTCCCTGGTAAATAGTACT GTGTACAGAACTCTCTACCTCACTGGGCTCTGGGCTGGAGCTCCTCCAGGAGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGOC
WI-7743e	106 C A	TTAAATGAGTGTGTTGTCAOCTGGGATTGGGAAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCAGCACTAAAGCAGTGGAC/CACAGGAGTCCCTGGTAAATAGTACTGTG TACAGAACTCTCTACCTCACTGGGCTCTGGGCTCGGAGCTCCTCCAGGAGGTCAGGAGAG GGGACAGACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGOC
WI-7743d	275 C T	TTAAATGAGTGTGTTGTCAOCTGGGATTGGGAAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCAGCACTAAAGCAGTGGAC/CACAGGAGTCCCTGGTAAATAGTACTGTG GTGTACAGAACTCTCTACCTCACTGGGCTCTGGGCTCGGAGCTCCTCCAGGAGGTCAGGAGAG GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGOC
WI-7743e	106 C A	GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCTCTCAGOC

WI-7743d	275 C T	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG TACACAATTCTGCTACCTGCTGGGCTCGGGGCTCGGAGCCTCATCCGAGGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106 C A	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGCTCGGGGCTCGGAGCCTCATCCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743d	275 C T	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGCTCGGGGCTCGGAGCCTCATCCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743c	106 C A	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGCTCGGGGCTCGGAGCCTCATCCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743b	275 C T	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGCTCGGGGCTCGGAGCCTCATCCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	106 C A	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGCTCGGGGCTCGGAGCCTCATCCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	275 C T	...	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGAGTCCCTGGTAAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGCTCGGGGCTCGGAGCCTCATCCGAGGCGAGGTCAGGAGAG GAGGGGAGAACAGCCGCTCTGCTGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7758	144 A G	...	TGACATTATTCAGAGTTAAAGCAACACTTACAGAAATTAAGAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTCAGAGAGCTGCTGTAATTAAGCAACAGAGTGCAGACATCATCAAGTG GAGAGAAATC(A/G)TAGTTTAACTGCATTATAATTTTATTAACAGAAATTAAGTAGATTTTAAAA GATAAATGTGTAATTTGTTTATTTTCCATTTTGGACTGTAAGTACTGCCC

WI-7765b	126	G C	ACAGGCGCTTTGCAGGTGCAGCCCCACTGCTTTGAOCTGCCCTCCCTTCATGATGAAATTCOCT TCATCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAGAAAGGGTCAGTATGG(GC)ITAGG GAAACATTCACCTCTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTG ACTCAACCAATCAGAACTTCTGCTGAGCCCTGTAATAAAGGTCGGA
WI-7773b	237	C G	TTAATTTACTGATCCAGCAAGCAACATCTGTATCAGATTATTTAAGTTTATCCGTAAGTTT GATAAAGATTTCCTATTCCTTGGTCTGCAGAGAACCTAATAGTGCTACTTTGCCATTAAGCA GACTAGGGTTTCATGCTTTTACCCCTTNNNNNNNTGTAAAGTCTAGTACCTACTTTTCTTT GATTCGACGTTGACTAGCCATCTCAAGCA(C/G)ITTCGACGTTTGA
WI-7774b	170	T C	TGCAACCTCTTTCGTGATGGGCGCCTGCTGGTCAGCACTCCAGTAGCGAGAGCGGCCAGCAAT CAGATCCAGCTTCGGCATTTGATGAGCAACAAAGAGTGTGTTCCCGGGGAGGAAACACTTTTAA TTACCTTTTGAGGCAACCCCTTAACTCTGTTT/CJATACCTGCTTATTAATGAGCGACTTAAA ATGATTGAAAATAATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGCCT
WI-7785c	165	G	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATCTGTAATGCAATGGAATAAACTGTCTCCCTCATGCTCTATGAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAAATTATTATATACATTTACCA TAAITTTTGTCCATTGATGATTTATTTTGTAAATGTATCTTGGTCTGC
WI-7785b	165	G	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATCTGTAATGCAATGGAATAAACTGTCTCCCTCATGCTCTATGAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAAATTATTATATACATTTACCA TAAITTTTGTCCATTGATGATTTATTTTGTAAATGTATCTTGGTCTGC
WI-7785	156	T	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAATCTGTAATGCAATGGAATAAACTGTCTCCCTCATGCTCTATGAACTGC ACATTGGTCATTGTGAATANN- /NNNNNNNGCCAGGCTAATCCAAATTATTATATACATTTACCATAATTTATTTGTCCATTGA TGTAITTTTGTAAATGTATCTTGGTG
WI-7789c	84	G A	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAGGAGGGCCACATCTACAGAGACTCTCC TGACGGTGGAAITTAAG(A)TTTAGGTCCCTAAAGCATTTGACACACAGATTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAATGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTGACTCGGGGCTGCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	G A	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAGGAGGGCCACATCTACAGAGACTCTCC TGACGGTGGAAITTAAG(A)TTTAGGTCCCTAAAGCATTTGACACACAGATTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAATGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTGACTCGGGGCTGCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73	G A	---	---	---	TCTCCCTCATCAACTCCGAAAGTCTGAATCTCCCAAGGAGGCGACCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAAATTTAAGTTTAAAGGTCCTTAAAGCAATTTGACACACAGTTGTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190	C T	---	---	---	AATGTCAGTCACCTTCTCAAAACCTTACAGTCTTCTTAAAGTTACTCTTCATGAGATTCATCAAT TACTAATACCTGTATTTTGGTGGACTAGGCTTGCCTATGTCTATGTGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAGTTGTCTTCTTCTTGAACCTC/TCTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	C T	---	---	---	AATGTCAGTCACCTTCTCAAAACCTTACAGTCTTCTTAAAGTTACTCTTCATGAGATTCATCAAT TACTAATACCTGTATTTTGGTGGACTAGGCTTGCCTATGTCTATGTGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAGTTGTCTTCTTCTTGAACCTC/TCTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	C A	---	---	---	CAGATGTTCTGGTAACTGAATGCTGGCAACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[G/A]GTCATCATCAAGAAATTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAAAGCCCAATATAAATGTACTTTTCTCCAGAAAATTTCTCTGAGGAAAATGTGCCAAA TAAGATGAATCACTTAAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7795	81	C A	---	---	---	CAGATGTTCTGGTAACTGAATGCTGGCAACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[G/A]GTCATCATCAAGAAATTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAAAGCCCAATATAAATGTACTTTTCTCCAGAAAATTTCTCTGAGGAAAATGTGCCAAA TAAGATGAATCACTTAAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7814c	41	G A	---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGATTTTCAATTTAGTCAATGTGACCCTC TGCTTTGTGTTTCCAGCGCTGCAAGTTCCAGGATGCTACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTTAGAGAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTTGTATTTTAAAGAAATAACAGAA
WI-7814b	41	G A	---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGATTTTCAATTTAGTCAATGTGACCCTC TGCTTTGTGTTTCCAGCGCTGCAAGTTCCAGGATGCTACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTTAGAGAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTTGTATTTTAAAGAAATAACAGAA
WI-7814	28	G A	---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCGATTTTCAATTTAGTCAATGTGACCCTC TGCTTTGTGTTTCCAGCGCTGCAAGTTCCAGGATGCTACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTTAGAGAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTCTTTCTCTGGTAAATTTGACTTTGTATTTTAAAGAAATAACAGAA

WI-7865	25 C T ...	---	---	CCACTTCCTATCTGATTTTCCAGGCTAAATGAGGCGAGGAATTCAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAGATTTCAGGGTGTCTTCCAACTGAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCAGATGCCTATGTAAAGGAAGTGCTATTACCCAGTAACCCCAA
WI-7865	191 C T ...	---	---	CCACTTCCTATCTGATTTTCCAGGCTAAATGAGGCGAGGAATTCAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTCAGGGTGTCTTCCAACTGAATCTCAATGTTCTCAGTA[CT]GAAAAAC CTGAAATCAGATGCCTATGTAAAGGAAGTGCTATTACCCAGTAACCCCAA
WI-7867c	92 A C ...	---	---	TTCAACACCTGTCTCCACCTCCCACTCTGTGCAATCACTTCCACCTTCAGCCTCAGTCTAGTCCCC CTAACAAATACCTGTCAAGAGG[AC]GAGTGCAGCTCAGGTGGATTAAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTTCTTTAAAGTAACCAATTTCTGTTCTGCTATAAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ...	---	---	TTCAACACCTGTCTCCACCTCCCACTCTGTGCAATCACTTCCACCTTCAGCCTCAGTCTAGTCCCC CTAACAAATACCTGTCAAGAGG[AC]GAGTGCAGCTCAGGTGGATTAAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTTCTTTAAAGTAACCAATTTCTGTTCTGCTATAAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ...	---	---	TTGATCGATCTTTTCCACCTGTCACTCAAGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CAACCAACCTGCTCCCTCTGATCCTCCATCAGGCGCCAGATCTTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[AC]TTAGAGGCGCCAGAAATGGGCAAAATTAT CACTACAGGCTTTGACTCAGGTTCCAGTAGTTCATTTCTAATGCTAGAT
WI-7868b	173 C T ...	---	---	TTGATCGATCTTTTCCACCTGTCACTCAAGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CAACCAACCTGCTCCCTCTGATCCTCCATCAGGCGCCAGATCTTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[AC]TTAGAGGCGCCAGAAATGGGCAAAATTAT CACTACAGGCTTTGACTCAGGTTCCAGTAGTTCATTTCTAATGCTAGAT
WI-7868	66 T C ...	---	---	TTGATCGATCTTTTCCACCTGTCACTCAAGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CAACCAACCTGCTCCCTCTGATCCTCCATCAGGCGCCAGATCTTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[AC]TTAGAGGCGCCAGAAATGGGCAAAATTAT CACTACAGGCTTTGACTCAGGTTCCAGTAGTTCATTTCTAATGCTAGAT
WI-7870b	85 T C ...	---	---	ATCTTTGCTCCTCGAAGAAATCAGCCATAAGAAAGCACTTAAATCTCTGCAAGTATTAGAGGG GTGGGTGGGGGAATCCT[CA]TTTATCAGACTCTGTGAATTAATGAATTAATGTTTACTCAGAGGA GCTGCAAAATTTGCTGCAAAATGAATCCAAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT CTTTATCATGAAGCAGATCAATTAACAGGCTGTAGACCCACCTAATATCAATTTG

WI-7870	76 C T	...	ATCTTGCTCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAGGG GTGGGTGGGCTGGGAATCCTATTATTACAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGAG CTGCAAAATTGCCCTGCAAAATGAAATCCAATGAGCACTAGAATATTTAAACATCATTAAGTCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C	...	TTAGTCTCATGCCACTCCCCAGGAGCAGCTGCGACTGACAGCTGGGGGGGGGCTCTCCCGCTG CAGCCGTGCGAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCCGGCCAGGGCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCAAGGCTGTCTTCCCGAGACACAAGAG
WI-7889b	54 C	...	TTAGTCTCATGCCACTCCCCAGGAGCAGCTGCGACTGACAGCTGGGGGGGGGCTCTCCCGCTG CAGCCGTGCGAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCCGGCCAGGGCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCAAGGCTGTCTTCCCGAGACACAAGAG
WI-7894c	142 A G	...	AGCCCCCCCCCAATATAACTGTATCCAGAGCTGTATGCTGTTTCCATACATGTTTGTACT TTTACTATATCATACATCAATTAACCTTATGCTCTATTGTTTGTGAATTTATTTGCGTATAC ATTATCA/GTATGTAATAATTTGCAATTTTATTGAAATTAAGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACCGCTATAGAGTATCCATA
WI-7894b	142 A G	...	AGCCCCCCCCCAATATAACTGTATCCAGAGCTGTATGCTGTTTCCATACATGTTTGTACT TTTACTATATCATACATCAATTAACCTTATGCTCTATTGTTTGTGAATTTATTTGCGTATAC ATTATCA/GTATGTAATAATTTGCAATTTTATTGAAATTAAGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACCGCTATAGAGTATCCATA
WI-7900e	84 C T	...	GCTCACTGTGACCCATCCTTACTCTACTTGGCAGGCCACAGTAAACAAGTGAOCTTCAGAGCAGCT GCCAAGCTGGCCATGCCCTGCCATTGAAACAGTGTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC
WI-7900d	128 C T	...	GCTCACTGTGACCCATCCTTACTCTACTTGGCAGGCCACAGTAAACAAGTGAOCTTCAGAGCAGCT GCCAAGCTGGCCATGCCCTGCCATTGAAACAGTGTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC
WI-7900e	84 C T	...	GCTCACTGTGACCCATCCTTACTCTACTTGGCAGGCCACAGTAAACAAGTGAOCTTCAGAGCAGCT GCCAAGCTGGCCATGCCCTGCCATTGAAACAGTGTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAAGTACATCTCTCAGATTTGAACAGTGAAA TATGATGATTTTCTGAGCTAAACTCAACTATAGAAGACATTAAGAAATC

WI-7901	33 C T	...	AGAC TTAGGTACAA TTGCTCCCTTTTATATAC/TIAGACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACTCCAGGCCCTTGGTTGGGTCGTCGTTATTTGGGGCAGCGCGGTGGTCTGT CAGTCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACTAGTTCTGT
WI-7901	271 T G	...	AGACTTAGGTACAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAAACAGATT GTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGACCT TTTAAACAACTCCAGGCCCTTGGTTGGGTCGTCGTTATTTGGGGCAGCGCGGTGGTCTGTCTAC TCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACTAGTTCTGT
WI-7926c	150 C A	...	CATTCCGATCTGTCAACAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAGCAAAAGTGATACAAACAGTAGTATTTGGGAATGCCCTCAT TACAAATGCAATACTTAC/ATTTTAACTCTTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATACAGAAATTACACTGTGGAA
WI-7926b	28 A T	...	CATTCCGATCTGTCAACAGGACAGAAATTTGCAATGGACAAAGGATGAGCTTTACAAAGATGATG ACTTTGGAGATCAGAAATTCATATTTAGCAAAAGTGATACAAACAGTAGTATTTGGGAATGCCCTT ATTACAATGCAATACTTACATTTTAACTCTTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATACAGAAATTACACTGTGGAA
WI-7926	150 C A	...	CATTCCGATCTGTCAACAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAGCAAAAGTGATACAAACAGTAGTATTTGGGAATGCCCTCAT TACAATGCAATACTTAC/ATTTTAACTCTTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATACAGAAATTACACTGTGGAA
WI-7947b	203 G T	...	AAGAGCCAGAGGTCAAAAAGGCCAACACCAATAGCAGCCAGCCACAGCCAGGCTCTGT GCTATCACAGGGTCACTCTTTACAGTTAGAACACCCAGCCAGCCACAGAAATCCATCCCTTCC TGAGTCATGGCTCAAAAATCAGGCCACCATTTGTCTCAATTCAAATCCATAGATTTCGAAGCCACA GAG/TJCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCAGCTGTGCCACCTG
WI-7947	203 G T	...	AAGAGCCAGAGGTCAAAAAGGCCAACACCAATAGCAGCCAGCCACAGCCAGGCTCTGT GCTATCACAGGGTCACTCTTTACAGTTAGAACACCCAGCCAGCCACAGAAATCCATCCCTTCC TGAGTCATGGCTCAAAAATCAGGCCACCATTTGTCTCAATTCAAATCCATAGATTTCGAAGCCACA GAG/TJCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCAGCTGTGCCACCTG
WI-7963b	145 T C	...	CATGTGCTGCTGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTTAAAAATAAAATGCC ACAAATTCATTTCTCTCTTAAGTATTACAAATGGAGTTTATCTGCTTAAAGTGGAGAAAT TGAGTGAATGAT/CJAAATTTTGTAAATTTAGGATAAGATCCAAAGTTATTTCCCAACTCTGTTTCCC CCATAAAGTTAGGCATGAGGAGGAGCACTATTAAAGGCAGAGAGCGGAAA

[illegible]

WI-8021b	57 C T	ACAATCTCAGAGGACTGTGGAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAAC/CTGATCCC ACGCTTTAGAACCTTACCACAGGAGTTTCTTGTAGTGAATCTCAAGTCTCAAGTCTTGGTAGGCATTGGA ACTGGTCTTTCACCTTGTGAGATTCTTCTTTCGGCTCTTATCAAGTCAGCACACACACACCTTTTCCAAG GATTTACGTTCGGCTTGTAGGGTGTTCGAATTCGGTGAATGGCA
WI-8021	57 C T	ACAATCTCAGAGGACTGTGGAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAAC/CTGATCCC ACGCTTTAGAACCTTACCACAGGAGTTTCTTGTAGTGAATCTCAAGTCTCAAGTCTTGGTAGGCATTGGA ACTGGTCTTTCACCTTGTGAGATTCTTCTTTCGGCTCTTATCAAGTCAGCACACACACACCTTTTCCAAG GATTTACGTTCGGCTTGTAGGGTGTTCGAATTCGGTGAATGGCA
WI-8024c	206 A G	CTGAAATTTACTATGCTCTCCACACAGAGCTCCCATTTTCCACAGACACAGTCAATGTGATGCA GCTTGTATTCAGGAGGACAGGGGAGGATCCAGTGGCACTTCCATGGGAAGACAGAGAGAGT GGGCCCCAGAGTGGAAAGACCCAGTGTATCACCACCAACCAATTCAGCCGCTTAGCCTCTAA TTCCGAGCTCTAGAACAGCTGGCCCTGGCTGCTCAGTACACAAAGGAAAGAGC
WI-8024b	206 A G	CTGAAATTTACTATGCTCTCCACACAGAGCTCCCATTTTCCACAGACACAGTCAATGTGATGCA GCTTGTATTCAGGAGGACAGGGGAGGATCCAGTGGCACTTCCATGGGAAGACAGAGAGAGT GGGCCCCAGAGTGGAAAGACCCAGTGTATCACCACCAACCAATTCAGCCGCTTAGCCTCTAA TTCCGAGCTCTAGAACAGCTGGCCCTGGCTGCTCAGTACACAAAGGAAAGAGC
WI-8077	187 A G	GAATGAGCCTTCCTAGCGCGAGGACCTGCTGCTGTTGGCCCTGCACATGCAATCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNATCTGCCAAACTCCTTTCT AAGGAGTCTGGGGTGTATGCTCCCTACAAAC/AGTTAAATCTCATCAGATGGATTTTATTAACTT GTTATGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGAAAGAA
WI-8118f	114 G C	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGTAAAGGAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAAATGATGCTTGTGCTTTTCTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCTTGTGACCAGTAGTCTTGGAGACTCAAGCTGAATGA
WI-8118e	40 A G	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGTAAAGGAGCTAT TATGTACTTTCATGCTGTGGAACCTGGCAATACAGAAATGATGCTTGTGCTTTTCTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCTTGTGACCAGTAGTCTTGGAGACTCAAGCTGAATGA
WI-8118d	118 T G	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGTAAAGGAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAAATGATGCTTGTGCTTTTCTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCTTGTGACCAGTAGTCTTGGAGACTCAAGCTGAATGA

WI-8118c	44 C T	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGAATGA(C)TCACCTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATAGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCACAGTTTTCTGATTTCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGACCAAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTTC/GGCAATACAGAATGAGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCACAGTTTTCTGATTTCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGACCAAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T	TTTTCTCTCTCCGGGGGACCAGGTACCTTTCTGGGCATACACATGGCAGCGCCCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGAGAGACCTCTTGGCACAC TTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCACGGCA
WI-8171c	46 A G	TTTTCTCTCTCCGGGGGACCAAGGTACCTTTCTGGGCATACAA(C)AGTGGCAGAGGSCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGAGACCTCTTGGCAC ACATTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171a	46 A G	TTTTCTCTCTCCGGGGGACCAAGGTACCTTTCTGGGCATACAA(C)AGTGGCAGAGGSCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGAGACCTCTTGGCAC ACATTTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCAC
WI-8171b	298 T C	TTTTCTCTCTCCGGGGGACCAAGGTACCTTTCTGGGCATACAAATGGCAGAGGSCCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGGAAGAGACCTCTTGGCACAC TTATGGAGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAAACAATCACGGCA
WI-8314b	85 G C	GAGGGAATGACATCTGGAGATCTAGGTATGTGGCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTTAAGGG(GC)GAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCAGCTGTCCAATAGAACTTTC TGATGATGAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT
WI-8314	78 C G	GAGGGAATGACATCTGGAGATCTAGGTATGTGGCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTTAAGGG(GC)GAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCAGCTGTCCAATAGAACTTTC TGATGATGAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCCT

WI-8321	178 G A	TTTTAAATATGCCGGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAAATGTGTCCAG TGTATATACCCAGGNAATCCATCTTGCTAGTCTTTTCAAGAGCTGCTGTATTACTGAGTCTCTGAGAAG TCCCCTTAGATAAGCTGCCACTTTTCAGTATGGTTCAGAATG/AJAGTATCTTAGTATCTTTCTTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGGCG
WI-8321	178 G A	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAAATGTGTCCAG TGTATATACCCAGGNAATCCATCTTGCTAGTCTTTTCAAGAGCTGCTGTATTACTGAGTCTCTGAGAAG TCCCCTTAGATAAGCTGCCACTTTTCAGTATGGTTCAGAATG/AJAGTATCTTAGTATCTTTCTTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGGCG
WI-8332b	123 A C	TATGTACTCACTTTTCAGTTACCCCGTCCTCCAGAATCGCATGTGTCTCCACCTGGGGGGCGGATATA AATTACCTAGATTGTCAAAGCCCGACTTTTCCCTCCGTGTCAGCCTTAGA/AJACTAAGTAG CAGTACTGTTGGTGTGTGTTTCTTCCCGCAAGTCCCTACTGCGCTACTTAGTACAACTAG AGGTGAGGGGNTCCGGGGAAGCAGTTAGTGAAGTGAAGTGTGATGCACA
WI-8332	114 A C	TATGTACTCACTTTAGTTACCCCGTCCTCCAGAATCGCATGTGTCTCCACCTGGGGGGCGGATATA AATTACCTAGATTGTCAAAGCCCGACTTTTCCCTCCGTGTCAGTCTGTCAGTCTTAGAAACTAAGTAG CAGTACTGTTGGTGTGTGTTTCTTCCCGCAAGTCCCTACTGCGCTACTTAGTACAACTAG AGGTGAGGGGNTCCGGGGAAGCAGTTAGTGAAGTGAAGTGTGATGCACA
WI-8378b	311 T C	TSCGGGCTTAACAGGAAGCATGACTGGGAGGCGCTCAGGAAGCTTATAATCATGGCAGAAGCGAAGG GGAAGCAAGGACCTTCTTCATGCGCAGGAGGAAGAAAGGAAGGAGAGTCTACACACTTT AAACAACCATGATCTCAGANTTCATCGGGAGACAGCATAGGGGATGGCATTAACCCATTAGA AACTGCCCATGATCAACTNTCAACAGGCGCTCTCCACAAGTGGG
WI-8378	308 T C	TSCGGGCTTAACAGGAAGCATGACTGGGAGGCGCTCAGGAAGCTTATAATCATGGCAGAAGCGAAGG GGAAGCAAGGACCTTCTTCATGCGCAGGAGGAAGAAAGGAAGGAGTCTACACACTTT AAACAACCATGATCTCAGANTTCATCGGGAGCAGCAGCATAGGGGATGGCATTAACCCATTAGA AACTGCCCATGATCAACTNTCAACAGGCGCTCTCCACAAGTGGG
WI-8426	184 T G	TTTAGACATATTTAGCATTAAGCCTCAACGATACAGCAATATGTTACATCTCTTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNAAATGTAACCTCCGACTTGTGCTTAATAGGATTTGACNTTAA GAGGNTCTTTGCTGTGGAGGGGTGGCTTTCCTTGAACCTTCATCTGTGJGCGCTGTGCTGGTGGT AGGCTGGAGTATGGANGNCCGGGGGCGCTTGGGNATNGMATCAGTGAG
WI-8450h	61 C A	TTGAGCCTCCACAATAATGCAACCAAGTTTTACATTTTTTAAAGCGCCTTCTACATCACTGCAJCA TGCTCTCTATCTTAGTTCCAAAGTTTAGTTTTCATCCCAATTACCAATCTGATTTATTTTAAGA AAAAACCTCCCGAGTTATTGTGCAAAAGTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATAGCAGGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55 T C	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATTCACACTCCAT CTCTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450f	108 T A	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450e	125 T C	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450d	125 T C	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450c	108 T A	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450b	61 C A	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450a	55 T C	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAAGCCCTTCTACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCAGTTATGTCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8458b	60 A G	CAAGGAAAGCTGTCAGTCTTCATAAATCTTCAAGAGTGTACAAAATACGTTATTTTAA/GICTA CAATTCAGGATAGCATCCAAACCTACAAACATGATGATACATTCGTACACACCATACACCTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTACCTGTTGAAACCTTTATGTCACAGT GACATCCATTCGCCAGACTTAATGTTTAAAGCAGCTGAGCAGAGTTCTCA

WI-9446	75	T C	---	GAAGCCTGATTAAGGGAGGNTTTATTTGATGTNAACCTACCAITCCATAGACTATAAGANCATTAT TAAAAAATTCCTCTAAAGNGACACATGCCCCAAATGACANGNCATAAAGCAACCTTTTAAAT TACTATCTTTTCATATGTGTGTGTGNCOCCTACTNTTATCAGCTGTCTCTGCTTTTGCTACCTA TGNGAAGCTGCACACTATCTGTGGCAATATGT
WI-9497b	185	A	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACTTTTTT GAGATAATTATTTAGATTCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTAGTTTACATTGA TATCTAGACATATATCTAAACAGTCTCCAAATTTNCCTTTAAATTAATCAAAAGTATGTTAATGTACATT GGAATTTCTACATGGAAAGCCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9497	185	A	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACTTTTTT GAGATAATTATTTAGATTCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTAGTTTACATTGA TATCTAGACATATATCTAAACAGTCTCCAAATTTNCCTTTAAATTAATCAAAAGTATGTTAATGTACATT GGAATTTCTACATGGAAAGCCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9523b	193	C A	---	GTGAAAAAGTTTCTATTCATTCATCCATGATACAATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTCAGAAAGTTGTATCTCATCATGCGAGTCACTGCGCATGATCTATGGTATTTCCACACATTGTACAGTG GACTCAGACAAATTACAAACTATTTTCAGCCATGATCTATGGTATTTCCACACATTGTACAGTG AAAGCTCTTCAGCTTGGAAACAACTTGTCAAGGCGAGCTGCATGCACATATAT
WI-9523a	47	GA	---	GTGAAAAAGTTTCTATTCATTCATCCATGATACAATAGATTGTGCTAAGGATCATTTTGGAAAGAT GTGCGAGCTTCAGAAAGTTGTATCTCATCATGCGAGTCACTGCGCATGATCTATGGTATTTCCACACATTGTACAGTG CAGACTCAGACAAATTACAAACTATTTTCAGCCATGATCTATGGTATTTCCACACATTGTACAGTG AAGCTCTTCAGCTTGGAAACAACTTGTCAAGGCGAGCTGCATGCACATATAT
WI-9554	202	T C	---	AAAAACAAAGTTTTCATACATCACAAAAACCTTCCATTATACACAGAAAGTGATTATACCCAGAC AAGCATCAGTGATGATCTACTGCGCTTTCCTAGTTGTTATTTGTAAGTCTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTACACCCCAAGTACAATATGATAAGCGACGCCCTCTGCAAGTG GTTCGCTGGATACCACTAAGAAAGTCTACTGCGCCCATGTTGGTTATGATTTT
WI-9555	97	GA	---	CCAAAGCCCAACCACTCATATGTTGGATTTCATAAACAATTTATGATCCCTTTTGGAGTAAGTAT AAATACCTTTTACATGGCTACCTTCTAAGGATGTTTGAATAAATCAATTTCAAGGACTCTTTAATCA GTTAAATATCTGCTTTAGAAGGCCAATAATGATCATCTCAGATTAAATATACAGTAAGTATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNCCTTCACATGATCACA
WI-9625b	172	A T	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCCTCTGGGAAAAACCTTTGGAAAAAACAACACGCACA TAAGTATCACTAAGCTGAGGGTTGTGGACAAGTTACTTCTTATGTTTACCAATTTTATTTGACATAA AGTAGCACAGACTAGTTATTTCAITTTAAAAAACACACTGACAAATCTTTTC

WI-9625	172 A T	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTCTCTGGGAAAACCTTTGGAAAAACACACGCACA TAAGTATCATCAACTGAGGGTTGGACAAAGTACTCTATGTTTACCAATTTTATATTGACATAA AGTAGCAGACACTAGTTATTCATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T	---	TTTTCTGAGATTCAAGAGCTACATTTTGGTTAGTGTCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTCACATTTAGGTGATGCTCTGTAAACAGTGTATTGCTAGAACCTAAAAATCCAAAGCT TACAACTTC/TGTCTCTTACCTGATACATTTATCCATTACTTTTCACTTTTGAATTTTAAAAATGTTA ACTTAATACGCTCTCTCAGATGTCCTGCTTTTAAATGTTT
WI-9676n	114 A G	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAATGATGGCTTTCTGCCC CCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCGATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTT
WI-9676m	184 G T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAATGATGGCTTTCTGCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCGATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTT
WI-9676l	84 A C	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAATGATGGCTTTCTGCCC CCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCGATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTT
WI-9676k	202 C T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAATGATGGCTTTCTGCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCGATGAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTT
WI-9676j	92 C T	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAATGATGGCTTTCTGCCC CCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCGATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTT
WI-9676i	173 T C	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAATGATGGCTTTCTGCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCGATGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTT

WI-9676h	134 C A ...	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTAATATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ C/AATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTG AGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676g	202 C T ...	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTAATATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGAGGQ C/TGAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676f	184 G T ...	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTAATATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676e	173 T C ...	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTAATATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676d	134 C A ...	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTAATATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ C/AATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTG AGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676c	114 A G ...	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTAATATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676b	92 C T ...	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTAATATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT
WI-9676a	84 A C ...	GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTAATATGCAGAGCAAGATGTGGCTTTCTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAATAACTTGA GGCCAGGGTCTCTCAGCTTAAAGCCTTGAATCCTATGCAATGTTGTTT

WI-9738b	40 C A	---	---	TGGACCAACACAGACAGATGATCTCGTGGCCCTGTGTA/C/AJATTACAACATCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCCACTTGGTGGAGCGGGTGGTTTTTCACTATGTGAGTACTA TC.TTTTATTCTGTCCTTATGTTGGTGGGCACATGCTGTATGCTGTC
WI-9738	40 C A	---	---	TGGACCAACACAGACAGATGATCTCGTGGCCCTGTGTA/C/AJATTACAACATCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCCACTTGGTGGAGCGGGTGGTTTTTCACTATGTGAGTACTA TC.TTTTATTCTGTCCTTATGTTGGTGGGCACATGCTGTATGCTGTC
WI-9756	47 A	---	---	ACTGAATGTAATGGCCAGGACCCAGGACCTTAAATATCAAGAAGTTAATCTGTGGGAAAA GAGTAACATAACAAAAGCATCTAACAGAGCAGGATGTGATGATGTCCTCCCTTATCATTAGTC AGTAAAGATAAGAAAGCCCTGGTGGATCCACTCCACAAACACACAGATATACACTTTTGAAG ATTCCACTTAACCACTGATCTCTAC.TTTTATGATTTAAACTCTCCGTGG
WI-9758	135 A G	---	---	GATGGTCCCTTAAGGATTGCAATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATCAAGAGAAATTCCTGTCGCAAGGTCAATTTTATACATTTA A/GTAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAAACCGCTGGTTTCTAAAT ATTACG
WI-9778	127 G A	---	---	ATTTAAATCCAGCGAGCGGGGAAATGGATACTTTCATATGCTCTGTACCCAACTATAAATTTTG GTTCTCATGACCATTTCATTGTCCTTCTCACTCCAAAGTACCACCTGATTTACCAATTTGACTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGAAATTTCTCTATTACACACTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A	---	---	TCTCCCTTTGCTCTCTCATGCCACTCCCTCAGCTGCACAGCGTTTCCTCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCCTGCAGGACTTGTGACAAATGCAGTTTC/AJTTGGATCCCAAGGGA CTCAAAAACAACTAGGAAATGGAGAAAGGAGCCTGGAAATCGGTGTGTAGCAAGCCCCAGGTGG TTTGTAGTGGACTAAAGTTTGAAGCCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101 A G	---	---	TGGAAAAATAGCTTTTATCATCTCTGATATGCTACATATGCTATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAATATAC/A/GTGTGTATGATATATATCTATTAAACATT AGGATTATACACACAATAAACGCTGTAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGATGTGTTACTTGATATGCTGTG
WI-9880c	222 G A	---	---	GAACTAACACCTTCTGCATGGATTTTCTTGATATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGGTTGAGTTTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCTTGGACTATAGATCTCTTTTAAATTTATATTTTATAAGCACATGAA AATGGAATGAATAATGA/GA/TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ...	GAACCTAACACCTTCTTGCATGATTTTCTTGATTTATGCGAGTTAACAAATAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC/CATATATAAGATCCTCTTTAAATTTATATTTTATATAAGCACAT GAAATGGAATGAATGAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ...	GAACCTAACACCTTCTTGCATGATTTTCTTGATTTATGCGAGTTAACAAATAAATGTTATTAGATC ACTGGTCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGAGTATATAAGATCCTCTTTAAATTTATATTTTATATAAGCACAT GAAATGGAATGAATGAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ...	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACTTGGGAATCAACTAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAACCAACGCCAGTTATCACAGTTTCTTNTTTTGTCTCTACCC ATTTCCATAACAAAGAGCTACACAAATTTGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGTCAATGAATGAATGATTCGAAA
FB25G10b	109	A G ...	TCCCTCAATGACAGATGAATTAATTTCTCTTGGGTAAAGAAATCTTTATGCCATTGTGATTAA AAGTCAGATTCAAGACACTGCTTTATGTACAGAAATGGAA/GTGTATTTTAGATCCTCCGCCAG TGACAAGTAACTGAACCTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A G ...	TCCCTCAATGACAGATGAATTAATTTCTCTTGGGTAAAGAAATCTTTATGCCATTGTGATTAA AAGTCAGATTCAAGACACTGCTTTATGTACAGAAATGGAA/GTGTATTTTAGATCCTCCGCCAG TGACAAGTAACTGAACCTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C A ...	ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGAACACAAATTA GATGAACCTGAAATTAAGNTAAATAAATAAAAT/CACAAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCTAATGAGATTTCACCTGGNCTCAAGTCATTTTGTAGTGA GGCATTACAAATATGACCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161	C T ...	CGTCTTCTCTTTTGTAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGTTGTCCC TACTGAGCTTGGGCCAGGTGTGTACTTAGGAACCCACCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCTCTGTGACACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTGTCC
S72904	51	G T ...	AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGGAGTCCCTTT/GTAAATTTGTCAGTTC ATTCCTGGAAAACTTTTGTAGTTAAATAAGGATCCTAGGACAGCACCTCGAAGTACAGGCCCTAAA GAGAAATTGCTCAAAACCAACAGTGTGTAACCTCCCTCCCTTTCTGTCAATGGTGTCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	TATCTTTTATCCTGGGCCACAGTCTTGATTATCCTCTGTGGTAAAGACTGAATTTGTAACCG CAATCAGATAAATGGCAGTACTTTAGGACACACACAAACACAGACCTTACACCTTTTGATATGTA AGCTTGACCCTAAAGTCAAGGGACCTGTGTAGCATTCAGATTGAGC
ESTC1	33	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGAGCAACAGCTAGGAAA
ESTC102	37	---	GCTACTACCAAGGCTGCTTGGTGGACAAAAAATACNAGGAGGATCCACGGGATTAGTTA GCCATCAAAATTCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC103	21	---	TGCTGGCTCAGTCTCCTCACANGCTGTATTACCTTTACAGAGCTGAGTGAGGCTGTGCT
ESTC107	20	---	AAAACAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGCGAGTGCACAGTGACC
ESTC109	35	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC110	23	---	AAGGGACACAGTGTGCTGACAAAGGTGACACTGAACANAACAGTTTCTTTAAATTGTAAAGCGGG CATCG
ESTC113	37	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAAGC CTCCA
ESTC117	24	---	TGTCAGCAGATCTTGAGGGTTATNGTTAAGCCTGATACAGCCTCTTT
ESTC119	24	---	GACAATAAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC122	34	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC123	21	---	GCAGAGGATCAGATAAGGCCCTCAGAAAGCCAGGCCCATNTTCCATGGGACCAGGCTGGCTCAA TGTGGAAGTGG
ESTC128	42	---	AGTCACCATGCCCAAGCCTAGNATGAGTTAGTAAGATTGGTTAGCTGGGGAG
ESTC129	20	---	GTGTATCTGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC13	46	---	GCCTGCTCACAAAGGTAGCAAAAAACATAAATCTCAGGAAAAATGAACANGAGAAGCTGAAACAAT CTACACCTGAATG
ESTC130	49	---	

ESTC132	30	GGTAAAGTCTAAATTACTGCCTTAGCAACNCTATGTTGTGAGGTTTTCGCTGCA			
ESTC137	21	CCAGTTTGGCTCTCTCTCANAGTCTCTCCATGTGGCAACA			
ESTC139	45	AGGACACAGCCTAAGGACATGAAGGTACAGATTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG			
ESTC14	20	GAGGAGG			
ESTC142	72	CCATTGTGGTACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCTTGCAATGGTTAGAAAGC			
ESTC143	29	TTGCCCTGGTG			
ESTC144	26	CTTAGGCTCATAACAATAACAGTCTCAATAACAAAGACGTAATACTATTTTATTCATTTTAAATC			
ESTC146	20	AAAGANACCATTCCATTCTCTAACAAACA			
ESTC148	42	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG			
ESTC149	28	AAATCCATATTTCTTGACATGAGGNGCTTTTTAGCAGCATTTTCGG			
ESTC150	20	CATGTCAGGATAAGGAGCANACACCAGGATTTATACCGGTGSCAGCG			
ESTC151	49	TCAGTTCAITTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG			
ESTC155	37	GGATTGTAATTTGCCAGCTTTGTAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT			
ESTC156	32	CCAGGAAACAAAGCACACANACTTATAGAATCTTTGGTTTAAAAATTTTCAATAATATCAATATT			
ESTC158	35	AAACCTGATGTTTAAAGAACCTAATGAGA			
ESTC159	31	GAAGCTAAGGCCCAATTTTCTTTTAAATACAAATCTACTGGTGTCTNAAAACCTAGAGCTTAGGA			
		AACACAGCC			
		TTTTTAATGACAACTCAATCTACATACATACAGTNTTGCAGAAATTATAAGTGGATCAACAATT			
		ATATTATTGATACAACTCATGAGCAITTTACA			
		GCAGCAATTTGTGACAGGAGAGGCAAAACAAANCTGGCTGCCCTGGGATGGAGCGGGGGCCCTCA			
		CCACCACCTGCAT			
		ACCAAGCCCTGGGATTACTGCTTGTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTACGTGTGC			
		AA			
		AGCTGGCAAGAGACTTCCTGAGGACATCAGNTACGTTGGTCAATTAGGCGACGGTCTGTTCTGCA			
		GCCTTGAAGG			

ESTC16	23	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGTGATCATCCCCACAAGGACAGGTT
ESTC160	38	TTCTAGCATTGCTGTGTCAGTGGGGGCTGAGCTGGGGGCGAGTGGCAGTGTCTACTGGGCGCGTTTG
ESTC162	36	GGACTGGGTTGA
ESTC164	31	CTCTCGTCCGTTTGCAAGTTGCTGTTTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC169	22	TCATTCTCCATAGAATATTGGTTTGTAAACANGAATACAATCCAATATATAACATTAACAATCC
ESTC176	23	GATACATACCA
ESTC177	42	GTCTCTGGTGTGCAGGGAATCANTTTGTGGATTAGAGGAAGGTGCGCGCTCTGTTTCCATGACTT
ESTC18	29	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC181	21	TGGGTGGCTCTTAAATACCTTCCAATATATTTTCAAAATTTTNCITTTATTTAAATACCTTTTAT
ESTC186	43	TCCTTTATTCCTCAATAAAAGGCAACCAA
ESTC187	24	TCAGACACTGCCGAGCATCAGCATTGTCNTGTACAGCTCCCTTCCCTGAGGGCGCCCTGGGAGAC
ESTC188	25	AACCTGGACAAGA
ESTC189	27	TAGGGATTCCAAGTTGCCCTGGNTTAAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC
ESTC196	42	CA
ESTC197	26	GCTTGTAGTGGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGTAAITGTCAITTCAGCTTG
ESTC200	44	ATTTTCACTCA
ESTC197	26	ACCATGATTGCTCTACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC198	25	TCATTTAACAGGGTTATGTACACACCTGTCAACCTCAAAACAGATGATCATCATCTTGTCTTCCAT
ESTC199	27	CTTGC
ESTC200	44	AAAGTACAAATCCAGTATATGCAGAAAGNTACTCAGGCATCAGCTCGTGATCA
ESTC201	27	TCCTCAAAATACCACITTCCTCCTAACTTATCAGTCTAGTAAGCNITTCAAAGGAGGAAAAATGGGTAC
ESTC202	42	CTTTCAGGGG
ESTC203	26	ATCTCAGTGTCTGCTGCCCTCCCGCCNGCAAGTCTCCCAACAGCACA
ESTC204	33	AAGATTAGGACAGACCGCGTATAGTAGCTCTGNGGAATCTCAAGAACTCTAGAGGGGCTGTGGAA
ESTC205	33	CGCTGCTTAGATC
ESTC206	44	TTTGGTGAATAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT
ESTC207	44	CAATTACTCTCTTTTGGCTGCAACAG

ESTC201	35	TCCTACTGGGTAGTTTAGCAACATTTTAAANCCACATCCACAGATTGGTT CTGCTGGAGGGAGGACAGACGCGNCAGCGGCTGGGTGGCGGCCGAGAAAGGCTGGCGGTGATGTT CGAGATGAGCC
ESTC202	22	ACACTTAACAGGTTAAATATCCAAATNAATTTACTGCAACTTTTGTAGAAATTTATTGTGCTAC AAGACAGTTGCA
ESTC203	27	TATAGCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATANAGCAATACTATTGTTTAAAGC CTAAGAGTGAATA
ESTC208	43	GATGAAGTGGCTTCTCTTGGCGAAAGGATNAGAGTGAGTGACCGTGACCTGTG GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC210	29	CTCCAGAGTCCTCTCTCTANACCAGGGGCGAGGGAGGTAGGGAAT TGGCAAGAAATTTATTACACTAACAAATTAATTAATCAGAGTATTNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC212	27	TTTGTGAGTAAATGAGCAATACACTGANTGGAAATCTGCATGATTAATAACATTAAACAAGTTTCAT AAACACACCCCA
ESTC214	21	GTACACATCTCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAGGAAGC
ESTC216	49	TCATTGAAGAAAAATTAGGGTTTATCTTATTCTAAATGNGAGAAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC217	28	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTTC TTGATTTAAAAACAGAAAGGGGAGGGA CGAAGGTAGATTTCCTCACATATTACAAAAATACANAAACACACACACACACACACACA
ESTC219	32	TGCACGTGTACTCCCGACAGCAGAGAGCTTACATACCATATAGAAAGAGCATAGTGCTTCAGAAAGGA ATGTGTAGGATCG
ESTC22	41	TTCTACTTTATTTCATATTCACACCAATACGACTCCTTTAAATTAACATAAAACCACATACAGGGT TCCTGAAGGG
ESTC223	27	GGTTCCTCCACGAAATTTGAAAGACATATTTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA CAAAAGGGTTAGTCATATTCGCCCANCAACAGCATGATAAATAATTC AAC
ESTC224	37	
ESTC225	20	
ESTC23	27	
ESTC230	43	
ESTC231	24	

ESTC28	23				GAAGAGCTGGGCACGCATCTGACNTTTCCTCTATTCTTATAAAATAAAGGAAGCAGAAATCT CC
ESTC3	20				CAGACATGACCTAACCGTCCCGGCCCTCAATTCATTTATCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32				ACAGCCCCACAGAACTATTGTAAACAATAATINICAGTCGGTGATCATTTGTAATATACATAAAG CAATTCCTCAGA
ESTC33	25				AGCACTCCAGCTCCTTGACGTTGTNGGACACAGGGAACCTCCGGAA
ESTC39	26				AAGGAAGGAACCCACCTGGGCTTNGGTACAGAACTCAGAGCCTGGGCAATTA
ESTC4	23				CCACTGAATCACACAACATGGACNAATCTCAAAATCATTTATGCTGATGGAAAGAAACCAATT
ESTC40	22				GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAATAATTTGACTTGTCCCCCTTCAC
ESTC45	37				TTTGAGGTTTGTGTGGAGTTTGTCTTTGTAAACNCCTCATCATCAGGCTATATATTA CTGTCCGTGGTGAGCCCTGCCGCTGTCCATGGGCCAGGAGCCACTGGTGGGANCOCGGCAGATG TTTACCCCTGT
ESTC50	56				GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC56	45				AAGTGGCCCTCCAGTCCCNCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC57	20				GAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC59	38				TCTGCAGCATTCTACTACCAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC6	27				AGTGATTTTGGTAGCGTGGTTCTCATCTGTGAAATTCACAGCGCAATGACAGANCCTCTCTCCG ACCCACTCAAG
ESTC61	57				ACAGACAGCATCACACANAGGGCCCGGAGGGTCGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC63	20				GAGAGGCTAGTCAGGAGGANACCCCTCAAGTTTAAATCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC69	20				AGTTTCCCTAGAGCTGTGGGCCAGATAGTGTTCCTGAGTTGCANGCACGATGGAGATTGGACACT G
ESTC7	45				

ESTC72	37	---	---	---	GGGTTCCAAATGGGTATGGGCCAGGAGGCTGGCNTTGGCGTGACGCCCTAAAAAGTGTGAOC AACAAATTCACAGCTACAGGAATCTAGAACAAAATCAAAATATTATCATCANTTGGGTTGAAAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTTCCTGTCCTCCATCGGAAACCAGAGTTTCCCCAGGNGAGCCCTTCCTATCTGCGGTTA
ESTC77	40	---	---	---	GGCTCAGCACAGGATAAGANCCGCCACTCCGCATGTCCOCAGAGGGCAGCACTCCAG TTTCAGATGATGGGGTCTGAGATGNTCTCAGGCTGCATCAGCTGCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGGTGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC83	53	---	---	---	ATTGCAAGGAAGTGGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTTCTCTGCTTGGCTTGGCATTCGCTCTCTGNGGCCAGTGTCCACCCAAAGTGTCTTCCCGATGAT
ESTC89	22	---	---	---	CTCCCTCTCAGTTCACAGTGGAGACTANGGAGATTACAGGGCAGGATCC
ESTC90	33	---	---	---	GCACGTTCTTTGTTCTCCCTCTCCAGAAAGTGNAGACGCTATTATTAGTTTGAATTATCTGTG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCTCTTAATTCA GTGGATCTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGCTTCTCCAC/TTGCCAG ATTCTTATCAATGATCTTACCTAAGAACAGCAAGATTCTGGCAAGCACACCGATCTAGAGATAC ATCTTATGCGATTTTTCACAAAAATCAAAAGAAAGAAAGAGGCTTAGCTG
DWU-100	127	C	T	---	TTCCATCTCTAGATATCTACTCAAAATATTGAGCAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTCAATGGCJAGGCCCTATTACAGTAGCCAAAGATGAAACAAACCCCAAGCTATATATACCA GATGAAAGGATAAACAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-177	77	A	G	---	CAAAATCCCTGGACTATCAACCTTGTGCTTAATCCCTGACAGATTCAAGGTTATCCATCTAAGTGAC ATTTTGAATTCACAGGTCGCCCAATCATGCCAGCTTCTGTCATATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGGACJTGGAACCAACCGCCTATCTGAGTCTTOSGCTCCCTCC
DWU-286	213	A	C	---	

DWU-252	94 A G	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGCTGCACAAAGGCATTCATGTAAAGTGT CAGAAGGAGCTACAAAACCTACCCCTCAJAGJTGAGCATGTGATCTTGGCCCTTTGAGGAACATCGGC TGCATTTGAAGATCCAGCTGCCTATTGATTAAGCTTTCCTGTTGAATGACAAGATGTGTTTTGTA AT
DWU-330	85 C T	---	GAACATTCCTCGAGCACITTCACCTACCAAAATGAGCATTAGCTACTTTTCAGAAATGAAGGAGAAAA TGCATTATGTGGACTGAACTGCAATCTTAAAGCTCTGAACAAAGCTTTCTTCTCTTTTGCAAA CAAGACAAGCAAGCCACATTTTGCATTAGACAGCTGACGGCTGCTCGAAGAACAATGTGACAGAA CTCGATGAATGTGTGTTGATTGAGAAATTTTACTGACAGAAATGCAATCCCT
DWU-370	231 A G	---	GAAATGTAAATTTGGCAGGTGAAAAGGTACAGATGCTGTAGCAGACCTTTGGTTTTAAAGAG AAGCATATTTCCCAACAGGCCAACTGTAGAAAGCCAGCTGAAGAGTAAAGGAAAGGTCTGAGG ACTGACCTGTGGCTGGCTGAAAGAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC ATTAGCGGTACCAATTCAGTGTCTGTTCCJTAGJGCACTATTTCCTCTGTGC CTCTAACTTCAGTCCCTCATCTATAAGATAAGGATTCACTTGATGACATAGCTCAGGTAATC CAGACAGAAACCCAGGAGCAJGTGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAGAAATCCAGTAAAGCAGCACACACTGGCTGA
DWU-1537b	89 A G	---	CTCTAACTTCAGTCCCTCATCTATAAGATAAGGATTCACTGTGTGATCAJCTATAGCTCAGGTA ATCAGGACAGAAACCCAGGACATGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAGAAATCCAGTAAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T	---	ACCATTTACTATGCGCAGTAAGTCCATACAGAAAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGAATCCAGGTCAGTGTCTCTCTCTCCCTCTGGGAAAT CAAGCCAGCTCCAGCCAGAAAGTGGGACTGTGAGGACATGAGGACTCGGCACCTGAGCTCGJAGA CCGCGACACCAACTCCTGAGCTTCTTGGGCCCTCTGAGTCTTGCTC
ESTD-ADAb	196 C G	---	ACCATTTACTATGCGCAGTAAGTCCATACAGAAAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGAATCCAGGTCAGTGTCTCTCTCTCCCTCTGGGAAAT CAAGCCAGCTCCAGCCAGAAAGTGGGACTGTGAGGACATGAGGACATGGAGCCCTCGJAGCAGT CCGCGACACCAACTCCTGAGCTTCTTGGGCCCTCTGAGTCTTGCTC
ESTD-ADAA	184 G A	---	TCTCCTGTCTTCTCTACTCTCATTAAGTTCAAGGTGAGTGAAGAACTGGGCAATTAACCAAGTAATCA TGGACTGCCCACTCGCAACAGAGGGCCAGTGGAGCAGGAGTATATGCTACGGCGTACCTT TTTTTATGGAGCCAGCACTGAGGCTTCJGAGCTCAGATGATCCTGT
ESTD-ANT1	160 T C	---	TGCCTGGGTGCAAGGCTGCAACAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCAOCCTCTTATCTACTTGATGTTCACATTTGGGGCTTGACTTTCCAAACACGGGAAG CATGTTTTCTCGGGCCCAAGAGGTATCTACCAJAGJATAGTGTCTATAGGCCATTG
EST10398-2b	168 A G	---	

EST10398					TGCTGGGTGGCAAGGTGCAACAGGAGGGAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA
2a	147 C T	AGATGCTGCCACCTCTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCAACACGAGGAAG
ESTD-C7	14 G C	CATTGTTTCTTCTTGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-					ATATCGTGGCCTTA[G]CJTACCTAGAGCTGGACAACTCCTGGGA
D4S95	90 T C	CTTTCATGCACGATAGCCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACATTTCAAGG
ESTD-					ATAATGGGGCAATCACCTTCTTCTTCTCTTCTTAGAGTCTACCGG
GPPK2L	38 G A	AGTCTCATCTCGGGTGTCCAGGTAGATCCCTTTACCC[G]ACCGAGAACTGCTCGATATC
ESTD-					CTGGCTGCCCCGACGAGCTGCTGGCACCTGGACGGCGGCCAGGCTCACTCTATAGTGGGGTGG
HRA5b	82 A G	TATTGCTCCACAAA[G]TGATCTGGATCAGCT
ESTD-					CTGGCTGCCCCGACGAGCTGCTGGCACCTGGACGG[G]TGGGGCCAGGCTCACTCTATAGTGGGG
HRA5a	37 C T	TCGTTATCGTCCACAAAATGTCATCTGGATCAGCT
ESTD-					GGAGGAGGAGGTGGGGGGGGTCTGCTCTGCTCCAGGTCCACAGACAGAGAGAGGGGCTCAGTG
NRAMP	81 A G	TATCCCCACCCCA[G]GTGGGGGCTGGGAGATGAAGAGGAGTGTGTCAGGT
ESTD-OTC	18 A G	GTGACCTCTCATTAA[G]AACTTTACCGGAGAGAAATTAATAATATGCTATGGCTATCAGC
EST38751					AGATCTGAAATTTAGGATAAAACAGAGAGGAGGTATGTAACA
7	36 C T	CCAAAGTCGTTCAATTTTAGCTTTGACGTTTAACTC/TGATCTATGGTTTCAAGTTAAACAG
					AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
					CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCCAAACTTTGTGGCTGAC
					TTTATGGCTAAGAAAGTTTCACTGGATGCAATTAATAACAAAT[G]JTTTACCTTTTGA AAAATAA
					ATGAAGGATTGACCTGCTGCTGCTGGAAAGAGTATCCGTACCGTCTGACGTTTGAACAATACA
EST40562	109 A G	GATGCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
					GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA
					GATTGACAGGTTTCATGACGAGGCTGTGACAGGATGAAGAGTGGCTGCTCCCTGA[G]TGGGAGCCAGT
EST18288					GTGGACAGCACCCCTGGCTTCAACACCTACGTCCTCCACTTCCAGGTAAGGCAAACTCTCTGCTGGCTC
3	121 C T	TGGCCCTAGGACTTAGTATCC
ESTD-AK-					GGGAGTGACACAGCTAGACGCAACCAAGGGGGCT[G]TACAGCTGTGTTCTATCGAGGACAGGCTTCT
168	31 C T	GCTCATCTGG
					AATCCAGCACTTTAGAGGCTGAGGCGGCAATACACAGAGTCAAGAGTTTGAGACCACTGA
					CCAACATGTGAACCCCACTCTACTTAAATACAAAATAGCAGGATGGTGGTGCATGCCTGT
					AATCCAGGAGGCTGAGGAGGAGAAATGCTTGAACCTGGAGGG[G]AGGAGTTGTGGTGGCCGA
ESTD-ALB	180 A G	GATGGCACCATTGCATCCAGCCTGGGCAACAGAGTAAACCTCTGCTTTC

EST70523 3	182 GT ---	---	TTCCGGCAGGCCCCCATCTCTTGGACCCCTGGTCCCCCTCAGGGGCCACCCCGGGCACTCACCCGCTCT CGCTCTCGGTAAACATCCGGCGGGCGCGCTCTTGAGCACATAGCTGACCGCTTCCGTATATAGGAGG AACCCTGTAGGCTTCTGTCCCGGGCCCTTGCAGGGGCCAGCCCTG/TACAGAGAGGGGTCCCTGT GGTGTAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
ESTID- APOA2	101 CT ---	---	CCAGGTTGTGCGACGCTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAACTCTTTTGAAC CGGGAGCGGAGGTTGCAGTGAAGCTGACATGCTG/TGCCACTGCACCTCCAGCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 CT ---	---	CAGTGTATCTGGAAAGCCTACAGGACACCAAAATACCTTATCATCAATTTGGTACAGGAGGCTT AAGTTACGATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAC/TCTAGAAATACACGAGAC CGAATGTATCAATGACATTCAGCAGGAACCTCAACGATACCTGTCTGTGAGCCAGGTTTATA GCACACTTGTCACTACATTTCTGATTGTGGACTCTTGTCTGAAGAACCCT
EST74167 6	137 C ---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAATCGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACCGGGACCGGCTGTCCAGGAGCTGCAGGGCGGCGAGCCGCTGGCGGGGACATGAGGGA CGTGGCGCGCGCTTGGTGCAGTAACCGGGCGAGTGCAGGCCATCTCGGCCAGACCGGAGGAGC TSCGGGTGGGCTCGGCTCCCACTGGCGAAGCTGGTAAAGCGGCTCTC
EST43211 8	132 C ---	---	CGCCTGTGTCAGTAACCGGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGCGGTGG CCTGCCTCCCACTGCGCAAGCTGGTAAAGCGCTCTCCGCGGATGCGGTGACCTGCAGAAAGCGCC TGCGAGTGTACCGCGGGCGCGCGCGAGCGCGCGCGAGCGCGCTCAGCGCATCCCGGAGGCGCTG GGGCGCTGTGTGACAGGCGCGGCTGGGGCGCGCACTGTGGGCTC
ESTID- AFSB	128 A ---	---	GGAGAAATGGAGCTGTGGGAAGGAGGCTCCGAGGGGTGGGCTTTTGGCAAGCCCTTCTGTGA AGCAAAATGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTCGACGTGTGGAAAAACCATCAGTGA GGAAGCCATCCCGCAGAAATTGAGCTGCTGCATAATATGACCCAAAC
EST36770 4	144 C ---	---	TGTAGCAAAAGTCACTGCATCATCATTTGGCTGCTGGCAGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGTATTTTGTGAAGAACCAATATTACAGTTTGTCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGGCTGGGCTGACCAAAAATATACTGGGTTTCTGTTTCTTTCTGTGATCAT TCTTCAAGTTATACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A ---	---	TAAATGAAGTCACTCACCAAGAAGCCCTGCACCATGTTTGGAGTTTGGTGCATGTTCGAAACCTGT CCATAAAGTAAATTTGTGAAGAGGAGCAGAGAACATCTCTCGAGCACTTCACTACCAAAATGA GCATTAGCTACTTTTCAAAATGAAGGAGAAAATGCAATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGAAGGCCCTAAAGAAGGCTTATG
ESTID- AFS11	29 A ---	---	GGGCAACATAGTGAACCCCATCTCTACATGAGAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGGCTGTGCTACTGAGGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGTAGGCGAAGTGTGCTACTGCA

[illegible]

ESTD- CB22	119 C T	GGCAAGTTTATTGATAGAGAGGAATCAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGACAGACATGGGAGTGCACCCATAGGAGCTGGATACAAAAG ACAGCAAGGAAGGGTAGAACATCAAGAGGAATAGGCTGGTGAACCCAAAGCAAGGAGACCT AGTAACATAATTGCTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	138 C	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACCAAGACGCT CTCAGAGCAACCTAGCCCAATTACCTCTCCCTTCCAGAGGACCTGAAAAGCTGTTCCACCCGA GGTCGCTGTTTGAACCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	145 A	ACAGGACCCAGACGCTCTCAGAGCAACCTAGCCCAATTACCTTCCCTTCCAGAGGACCTGAA AAAGTGTTCACCCAGGCTGCTGTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAAG GCCACATGGTATGCTGGCCACAGGCTTCTACCCCGACACGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGGTGCAGCACAGACCCGACGCCCTCAAGGAG
ESTD- CB25	146 A G	GTTTCTTCAGACTGTGGCTTCACTCGGTAAAGTGTCTCTCTTTCTCTATCTTTCGCCGTG TCTGCTCGAACAGGGCATGGAGATCCAGGACAGAGGCGTGAAGGCGCCAGAGCCACCTG TGCACAGGTAGCTTACATGCTGTTCTTGTCAACAGAGCTTACAGCAAGGGGTCTGCTGCC ACCATCCTCTATGAGATCTTGTAGGGAAGGCCACCTGTATGCCGTG
ESTD- CB27	125 C T	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTGTGTGGCCCTGGTTGCATTTACAGAGTGTCTGTGGAGTCTGCTCATCATCTGACCTATCTC TGATTAAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCCACCCAAATGCT GCTTCTCCTGTTCATCCTGATGAGGAGTCTCAACACCCATTTCCATACC
ESTD- D4S338	59 A T	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/ATATGTA TTCTTAACAATAAATTTGAAAGTCCAAATTAACCTTGTATCCATGGAGTGCAGAAATAATGTTA TTTTAGTGTGAGAAACAATACTAATCTTGATATGTTATCAGAGCCCTTGGTGACCCAGGTGA TTGCCAATAAGCAGTAATATTTTGAAGGAATCTGTCTTCAATGCAGTAG
ESTD- CYP206	61 A G	CAGGCGAGCGTGTGAGGTTGTCACCATCCCGCAGAGAACAGGTACGCCACCACTATGQAGCA GGTCTCATCAITGAAGCTGCTCTCAGGGTCCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG AAAAACAATTTAACAACCTTTTCAATCATATACACCATACATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTAAGTCAATCTAAATGTCTAATGATTAATGCAAGTTCAACAG ACAACTTCCCAAGCATCTACGATCAGAAAGGTGAAAATATTACATATCTGGAATTAATATGCCCA TATCTGCATGTC
ESTD- D11S1873	40 A C	CATCCCAAGCCCACTCTTAGCCACTGGCATTTTGGCGCCTCTGACAGATACACTCAGGGCGGT CATGCTGCACATCCAGGGGGCCCTACCTTTGTATGTCATGGGAAAGGCTCTCTGGGGGGGTG GGGTGTGGCTATGGTGGTCTGTGTAGAC/CTGGGGGCTTGGTTTCAGTTGCACTATTGCGTT ATTGCAGATTGCTTTGCTTTCCACTGAGCGAGCCCTC
ESTD- D17S33b	169 C T	

ESTD- D17S33a	75 C T	CATCCCAAGCCATCCTCTAGCCACTGSCATTTTTGGCCCTCTGACAGATACACATCAGGGCCGT CATGCTGCTACATCCAGGGGCGCCCTACCCCTTTGTAGTCCATGGGAAAGGCTCTCTGGGGCG GTGGGTTGT ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCCTC
ESTD- D18S8	133 A G	TTTGAGACCACCCCTGGCCAAACATGGCGAAATACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGGTACATGCTCTATCGTAATCCAGCTACATCGGGAGGCTGAGGCGAGGAAATGCTTGAACCCQA GJGGAGGCGAGGCTTCAGTGAAGCCAAAGATCACACCACTGCACCTACAGCCCTGGGTGACACAGTGGAA GACTCTGTCTCAA
ESTD- D3S11	44 G	AACCTGATTAGAACCTGAAATATACATATTTTATCTGAAAAAAGTCGAGTTATGGCTCATCACATTGG AATTTTGCATCATTAAATAATCCAAATAGTACACTGTAAATAAGAAATTAACAGAAATATCATTTGT TTATCAAACTATTATACATTTATTTATTTGTAAGCCATACATAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G	AGGTTCCACATTAATGCTGATGTTGCTGATGTTTCQJAGJGGAGCCTTGATGTCATCTGTATCTCCT CAGGTATCCACCTTGAGACGCTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTATTAATTCAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTTATCAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTC AGAAAGTGAACATACACTGCTCTAGAGCCAGAGTCACTGGAATGTTCTGTTTCTGGTCTTACGATGG CAGGTATGAATATAATAATCTGTCTTTTATTTGGAAGGATGCGCTGTGTGT
ESTD- D3S2a	248 G	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTTATCAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTC AGAAAGTGAACATACACTGCTCTAGAGCCAGAGTCACTGGAATGTTCTGTTTCTGGTCTTACGATGG CAGGTATGAATATAATAATCTGTCTTTTATTTGGAAGGATGCGCGTGTGT
ESTD- D7S399	83 A G	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCCTGAAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGJGTCTCTCATCATCCTTTTCAAAACATTTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTTCACGTGTGCTCAAGCAGCTGCTGCGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGGAGGGAGACA GAATGCTGATTACCTCTGTGGAGAACCAAGACTTCTGGGCTGTGGGTAGGGCAGCTGCTTCCAAAG ACCTCCTGATTGTAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT
ESTD-DMb	66 C G	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTTCACGTGTGCTCAAGCAGCTGCTGCGCTCCACT GJTTCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGGAGGGGAGA CAGAAATGCTGATTATCTGTGGAGAACCAAGACTTCTGGGCTGTGGGTAGGGCAGCTGCTTCCAAAG CCTCCTGATTGTAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T	TCCGAGCCATCGTGCATATTGGACTATGACACTGACGTCTCTCTGGAGGAAGATCCAAACCCATCAC ACAAAGGGTCAGCACCCAACTGAACCTGCAGATGCAGATGAATCCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C	TCTGCTTTGGTCAGGAGGCTGCCCGCGGAGCCAGAGCTGGAGATGAGATGCTCTCCAGCACCA GCCACCCGAGAGAGACCCGGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCGG TCCCACCGGCTCCACAGCACTCCCGACAGCCCGCCCAACACAGAGAAGATGGGCGATGCCAAAG ACCACCCAAAGATTGCCAAGATCTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T	AAGCAGTGGCCAGGATGAGCGCGCAGTAGGAGGGCAATAGTAGGATGTGGCGGGCCCTGGCTGG CAGCTGTGAGATCTCTGCCCCACAGGTGTAGTTACAGGTGGCTTACAGCTGGCTCAGAGATGCC ATAGCCACAGGGAGGTGCGTGATGCCAAGGGCTTCCTGTGAGGAGA
ESTD- ERB2	93 C T	TCTTCAGGATCCGATCTGCGCTGGTTGGCATCGCTCCGCTAGGTGTACGGGCTCCACACGCTGG GGTGAGGGGGTGGTGGGTCAGTGCTGGGGGGCGGTGCAGACCCCGGGCTGGAGGACTTCA CCCCGCTCACTCCGTTCTCTGCAGCAGTCTCCGATCGTACT
ESTD- ETS2	43 A G	ACTCACAGTCTTTAAGTGAATAATGGTCGAGAAAGGACCACTAGGGAAGCCGCTCTGGCGCCTG GCAGCTCTGGGAGGGATGGTTCTGGCTGTTGAGATCTCAAAGGACGAGCATGCTGGGACACA CACAGACTATTTAGATACTTTCTTTGGCTTTTGCACACCAAGACAGCAAACTGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCAATTCAGAAAGTTAGTTG
ESTD-F9	111 A G	AGATCCTGATGATTTTTCTCTATTTTTCTAAATGTTTACAGTTGAAGTTTATAGATTATGCCCCA TGCTCCATTTGAGTAAATTTGTGTAAGTATGATGTTTAAAGTCAAACTTCATTTTTTTTTTC ATAGGTATGCCAATTTATCAGACCAATTTGTTAAACAAAAAC
EST68787 5	144 A	CTTCTATGGGATTGACTTTATTTCTCAATGTTCTTACCTTTAAGAGGTTTAATATAGTAAAG GAACTTTGAGCTCATGAATTTGAAGCTGACAATTACACAGAAGGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTCGAACATTTGAAGTTGTTTTGAAGTTGTTGCTACCTTTAATACAAACCTAG CAGACGGAACCTGAACCTCAGGGTAAAGAT
ESTD- G00H	200 C G	CGCAGACCGGTGAGTGGGGTGGGAGTGTGAGGGAAGGAGGAGAACTGGGGGTTTAGGGACT TTCCGGGTGACTTTCCGTTCTGCTTGCAGAAAGGCGGAGAACACAGACCACTGGCTAA GTGAAGGGAACCTCTGTGTCGACCGGTGTTCTGCTGCCCTGTTTACGCTGTCTGTGCGCGAGTGC GACTCTGTCCCGGAAATTCGAGAGCT
ESTD-G00K	88 A G	GTTTTATGATGGCAGCTCTAATGACAGGATGGTACGCCCTGCTGAGGCCACTCTGGTCCCATGAC AACCACAGGCCCTCTCAGGAGACAGTAAAGCCCTGGCAGGAGAAATCCCCACCCACACTGGC TGGAGCAGGAAATCCGAGCGCGGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTGC ACCTGCAAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG

EST34088 2	62 A T	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCGAGGGTATAAAGGGGGCCACAAAGACCGGCTC[AT] AGGATCCCAAGGCCAACTCCCGGAACCACTCAGGGTCTGTGGACAGCTACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G	---	---	GACCTGAGTACCTCCCTAGTSGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC[AG]GGCATCA TTGAACCAAGTTTCCGGTCAAGACTTTGAATTTACGGTAAGTGCATGGTTCCTTAGG
ESTD-HT2	154 G	---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAGAGATGTGTACAGTTTGTACAGAGATAAAAGGATAAOCCTGGGGTTTTCTGTGC TTTGCTTCTTCCACATCCCTGGGGAGTTAATAGTGCATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTGTGAGTTTTCAAACAAGACACACTT
ESTD-HT5	149 C	---	---	AACACAAAGCCCCAGCGAGATTGAACCTCGGACCCCTGGTTTACAGACACAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTTCTTCTTCACTATAGATTGATGTTATGCTCTTA GCATTCGGGTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATCTCTACAAAATGAAA ACATTTCTGCTCTGTAAATCCCTCGAAAAGGTTCT
EST37382 5	124 A G	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCACCCCTCTTCTCTCCCTTGGA CTTTGAGTCAAAATTGGCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGG[AG]GCCCAGA AATCACAGGTGGGCACGCTCGCTACCGCATCTCCCTCTCAGGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCAITGCAACGGTCTTGGCAGGAGTGCTCTGGGAGAGAAAGGAGATG TTCCAGGGCACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C	---	---	TTTACTATTTCAATGGATACAGAATTGTGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTGCTTACATTTGTGGAGTGACGGGCGAGTGGTGGATCCGAGAGTGTGGTGG TGACCGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAACCCA
ESTD-IL1A	110 A G	---	---	CAAGTAAGCACCCCAATAAATGTAGCTATTACTATCATTTATTATTATTTATTTATTTTGT AGATGGAGTCTGGCTCTGTCACCCAGGCTGAGTGCAGTGCG[AG]CAATCTCGGCTCACTGCAAGCT CTGCTCTCTGGTTTCGCCATCTCTGCTCAGCTCCCGAGTAGCTGGGAATACAGGCAOCCGOC ACTGTTCCCGGCTAATTTTGTATTTTGTAGAGAGCGGAGTTCACCGT
ESTD-IL1B	99 A G	---	---	CCACTTACAGATGATTAATGGTACAATGAAGGCCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGTCTCTACCTTGGGTGCTGTCTCTGCTCAGGGAGCTCTCTGCTCAATTGSCAGG
EST74082	134 A T	---	---	TCCAGGGTGGTGCACCCAGGCCAGCTCTGCAGCAGGAGGAGGCTGGCTGGCTGCTGGAAGCATG TGGGGGTGAGCCAGCGGCCCAAGGCAGGCGACCTGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA TCCAGATCACTGTCTTCTGOCATGGCCCTGTGATGGCCCTCTGCCCCCTGCTGGCCGCTGCTGGCC CTCTGGGACCTGACCCAGCGCAGCCCTTTGTGAACCAACACCTGTGTGG

EST45311	151	C T	---	---	GGCCCTCTCTCTCCAAATCTGTCCTATAGTTTCTCTATTAAGTGAACATACATGCAATCTTTAGT GGATAGATGCACACAAACACAGCCATTATGGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCTACCTCTTTTAAACAGCCCTTATCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTCTTGTGAT
EST6258	80	A G	---	---	TGCCCATCAGCGGCCGAGAGCATGGCTTGCACAGCTCTTGAGGATGTCACCAATTAACCAAAAT CCAGTTATTTCCGAGGCCCTCAAAATGACAGCCATGGCCGCCGGTCTCTGGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGACAGCTCTTGCAATGGAGACTTGAGGAGGGGCTTGAGGTTGGT CAGGTTAGGTGCGTGTCTCTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216	26	A T	---	---	ATGCAGGATGAAGTGGACAGGGAGGATGAGGGCCCAACCTGTCTATCCAGGGGCTGCAGATGTCTG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149	G T	---	---	ATACTAGTACAAGTGGTAAATTTTGTACATTACATAAATATTAGCATTTGTTTGGCATTAACCTAA TTTTTCTCTGCTCAGAGCTGTAGCTTTTACCTTAAGCTTATTTTAAATGACAGTGGAAAG TTTTTTTCTCTCTGTAAGTGGCCAGTATCCAGAGTTTGGTTTGGAACTAGCAATGCCTGTGAA AAGAACTGAATACCTAAGATTCTCTCTGGGGTTTGGTGCATGCA
ESTD- KRT10b	183	C T	---	---	CCAAAGTTAAATAGTATGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAGGAAGAAAATGCAATTTTAAAGTAACTGCTAAGGTTTTCATTAAACCACCTATTACTTCTAAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133	A G	---	---	CCAAAGTTAAATAGTATGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAGGAAGAAAATGCAATTTTAAAGTAACTGCTAAGGTTTTCATTAAACCACCTATTACTTCTAAAG GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGCTTTTAAATAGT TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231	C T	---	---	ACCTCACCCCTCCCTTAGCCGCTGGGAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGGCTCAAGACTAAAGAGGGGCCAGAAATTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCCGTCTCAGGTTTACCACTGTGTCAACATTGACACA
ESTD- KRT8a	21	C T	---	---	ACCTCACCCCTCCCTTAGCCGCTGGGAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTCTAGAG TTTGTAGAGGTCAAGGGCTCAAGACTAAAGAGGGGCCAGAAATTTAAGTACAAAAGTGAGGCCCAT GGCTGCTATCTCTCCCGTCTCAGGTTTACCAGTCAACATTGACACA
EST75099	82	C T	---	---	CACCTGTGTCTAGATCTCTCAGTGGCCGCTCTACTGGTGTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAACTGTGGGGCAACCGGAGACCATCTTGGAGGATGAAGAGGCTGGCCACC CCCTCTCTCTGGCCGCTCTTGAAGTGTGG

ESTD-PAR	120 A	CTCTCAGGAACCAACAGTCTCTACCAACACGACTATTGCTGTCGAGAGGTACAAACCGTAGA
ESTD- Per/RDS	74 A	G	...	ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGCTCTGAAGACATGGAGATACGCT
EST68308	29 C	T	...	AATCGACTGGCTTCATTAGCTCTGTGAGTGTCTTCTTCTCATTCTGCTGTCTAGAACGTTTCTAG
5				GACTGGCAGTTTAAGCTTTCACCTTAGCTTCTGTATACCATGCC
EST54045	39 A	G	...	ACCTACAGACGTGCTGGATGGTGTGTCACACCCGAGGAATCTGAGACGAGACGAGGCTGGCTG
6				CTGGAGAGAGAGCTGCGGGAGACCTGGAGGGCT
				GGAAAGAGATTAAAGAGCTTGATTTGGAC/TJAATCTGTTCTTTGAGTGTGGAAGAGTTTCATGTC
				TCTGCTGAGTTACACAGAAATCCTTTAGTAGACGCGAGTAATAGATATATTCGACACAGATGGGAAT
				GGAGAAAGTAGACTTTAAAGGTAAAGAGTAGTATTTT
				GGAAATTAATAATAATTTAAATACCTCCATTTGCTT/GTCTCTTTAGTGAAGATGATACCTGC
				AAAGACATGGCTAAAGTTATGATTTGTCATGTTGGCAATTTGTTCTTACAAATCGGATGGGAA
				TCTGTTAAGTAAGTACTGTTTGGCTTGGATTTGATTTTAAAGTTGATCTTATCAT
ESTD- PXMP1	88 A	G	...	ATGAAACATGGTCTTTAATTTATGATATGTTTGTATAGTATCTTAAAGGGCTCTTTTTTTTA
				ATGCAGAAAGAGGGGAAAJA/JGAGCGAGCTGTGTGACAAGGTGTTTTCTCAAGGCTCATAC
				AGATTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAGTCTTATGAAATTTAATCTT
				CCCGAGGAATCTGAGACGAGCGAGGGCTGCTGCTGAGAGAGCGCTGCGGAGAGACCTGGAAGG
				CTTTCTGAGAGTGTGAAGAAGCTGGGCAAGGGCAACAGGTGGAAGCCGAGGCGGACGACAGG
				CCAGCCCCAGAGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCCT
ESTD-RDS	127 A	CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- s14544	94 G	T	...	TTGGGAAGTTAGAGCTATATTAATACGGAATTAAGGAGGACACAGAGGCTTAATTGAAAA
EST52908	45 A	C	...	TATCCCAAAGTTGAAATGTCTCAGTTC/GTCTGTGTGGGTTAGATGCGAGGATTTATATGATCCGTTA
				ACCTCT
				ATCACAGGCTCTGTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/AGTGGTGTGCAAGCCCTT
				TGGCAATGTGAGATTGATG
				AGGAGAAGCTGAGGGGAGAGAGACAGAATGACATTGATGATGAAGATGTC/TGGCTCAG
EST19590	55 C	T	...	GATGCCGGAATGAC
EST76136	39 C	T	...	TGAAGCTTTCGCCACCTTGCATTGTTCTAGGAGAACCT/CTGCTCATACCTTTATCTATAGCCTT
				CCCTAGGCTCT
ESTD- SPTB	176 C	T	...	TGAACACCCCTGTGGTCCGAGCCAGGTGTGTTTCTCTGGAGCCCTGAGAGATTGTTGTGTGTG
				CAGTCCCGCCGACCTGCTGGTGTGAGCTGGACATACACCTTCACTCTTTGGCCGAGAGAC
				ATTACCCACCTGGCCATGTCCCTGGCTGTGTGTCAC/CTGCTCTGGAAGACCCCAACCCCTGC
				CTCCCCCAACCAAGCCAGTTTCTAGCAAGGGCAGGAC

ESTD-TAT	224	C	AAATGGTGAAGACCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGATGCTAAGTCAGCACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCAGCTAGAACGTTTGTTTACAACTTTCTCCAGTATGGATGGGATATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THB	125	A	C	TGCGGCTTTCTCGGCGAGGGTAGACTCTTACTTGCTGTGATTTCCAAAGAGAAAGAGTCCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACAGGATC(A/C)TTCTAT CCACACTGGATTGCCCCAAACAGTCTGAGTGGAGCCAGGACTCAACGGTCCCGCTGTAGATGGG TAGTGAAGTTTTCATCTCTCTGCTAGCTTCTGGATTCTTTGCCACCGCAACAAGAGTCTATGC CAAGGCAAGAAAGCTGGTCTTCATGGGCAAAATCAATGCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATGACACATAATATGCATCCAGACAAAGAGGTCAATAATATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTCAATTTGGCCATAGTCCCTATGGGGATGACA
ESTD-TYR	122	G	T	AGTAGTGATGAAGCTAACAGCCCTCTCCTCACTGATCATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCAATAGTATCACA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTTCTTTCACITTTATTACCTTCTTCT AATACAAGCATATGTTAG(A/C)ATTAAAGTTCTAGGCATACCTT
ESTD- TYRP1	222	A	C	AGTAGTGATGAAGCTAACAGCCCTCTCCTCACTGATCATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCAATAGTATCACA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTTCTTTCACITTTATTACCTTCTTCT AATACAAGCATATGTTAG(A/C)ATTAAAGTTCTAGGCATACCTT
ESTD- TYRP1	222	A	C	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAGGTCAAGAGACAGGAAACACCCAGTG ACTCTGAGATGTC(A/C)TCAGACTGAGAACCCCGTTATGTACTGTTATCGACAAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148	C	T	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAGGTCAAGAGACAGGAAACACCCAGTG ACTCTGAGATGTC(A/C)TCAGACTGAGAACCCCGTTATGTACTGTTATCGACAAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148	C	T	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAGGTCAAGAGACAGGAAACACCCAGTG GTGACTCTGAGATGTCACCAAGTCAAGAACCCCGTTATGTACTGTTATCGACAAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74	A	G	

ESTD-SSA1	111 C T	...	TTACATTTGGATTGTTCTTTTGGCTGCGAGCACCTTTTCAACATGATGTGATCCCATTTGTCGAAGTTTGGCTTGGCTGCTGCTGTTGGGATAATTTGAAGAGATCTTTTGGCCAGTCCCAATGTCCTAGAAGATTTCCCAATGTTTCTTGTAATAGTTTCATAGTTTGAGGCTTAGATTTAAGTCTTTAATCCATTTGATTGATTCTGTA
ESTD-RVRI	109 A G	...	CTTCGTGACGGGAGGTACGTCTCCGCCCTCTTTCATGACATATGATGAGTGTGACCATTTCCCTCTGCTGACAGTGTGACACGGAGACTTGTCTACTATGAGTGGGAGCTGTGTGACATCTATGCCCGCTCCTGAGGGCTGGAGCCACTGAGATCAGCTGAGTGGGAGCCACCTTGGCTGGGGCCAGCCACTCCGAGTCCGGCATGTACTACCGGGCAGTACCTAGCGCTACCCGAGG
ESTD-WT1	70 A G	...	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCCTCCCTCTTCTCTTCTCTCTGCTGCGATGTGAAGAGTGGCCGATGCTGGAGTAGCCCCGACTCTTGTACGGTGGCATCTGAGACCCAGTGGAGAAAGGCCCTTCATGTGTGCTTACCCAGGCTGCA
ESTD-F2 EST44438 7	100 C ... 62 C T	...	GATAAGTACACTGAGGCCCGCCAGGAGTATTGCTAGTAGCCCACTGTGCTGACGCTTAACTCTGTGATAGTACACTGAGGCCCGAGAGCTGAGGGGATCTAGGGGATGGGTGAGGAATGGCCGCAACAAATGGGCTCCAAAGCCCGTAGGGGAACTGGGGGATCTAGGGGATGGGTGAGGAATGGCCAGCCAGTCCCGCGGTGGTGGTCCCAACAGAGAGGGCGGTGGAGGAGGACAGAGGATGGGC
ESTD-PBDA	103 A G	...	TGGATGAG. GCAGCCAGGAGCGGCTGCACCATGCCCGCCCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TJS TCTGCTCCGACCTAAGCGGAGAGCGCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G	...	CCTTCTCATGCCCGAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAAJAJTCTTACCCGAGCTTGTCTGCGCATACAGACGACAGTGTGGTGGCAACATTGAAAGCCCTGTAAC
ESTD-CTLA-4	48 A G	...	TGCAAAACACACAAATCTCTCCAGATGCCCTATGGCTGTGGAGCAGAAATATGGTCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGTGGTCAAGTCCAAGCCATTGGCTATCTCAACACTGTGTGAGTGTACTTGTAGTAAAGGAACTTGAATGTTATTCAAC
ESTD-ACE	96 C T	...	TGGATTCCAGTAGTTTCAGTTACTTATGAATATTATGATACITAGCTTAG ATGGCTTGCCTTGGATTTCAGGGCAGACAGGCTCAGCTGAACCTGGCTJAGJCCAGGACCTGGCCCTGCACTCTCCTGTTTCTTCTCTCATCCCTGTCTCTGCAAGAAATGCAAGTGGCCAGCCCTGCTGTGGTACTGGCCAGCAGCGGAGCATCGCCAGCTTGTGTGAGTATGCTCTCCAGCAAGCCAC
EST54419 8	88 A G	...	GATCAAGCAGTGCACACGGGTCAAGATGGACAGCTCCACAGTGCACCATGAGATGAGTGGCCATATACAGTACTACCTGCAGTACAAGGATCTGCC/C/TGTCTCCCTGGTGGGGGGCCAAACCCGGCTTCCAAGAGCCATTGGGGAGCGTGGGCTCTGGGCTCTCCCTCTCCACTCTGCAACATCTGCACAAATTCGGGCTGCCTCTGCTCAATTTGAATGATATTGTGCTGTGGGACCTGAGCAGCTTTTATGACCAAAATGATCACTATTTCTTGACCCCTACTTAQJAJTCTCTGGGAGATGTAATTTGGGTTTAGCGTGGTGTGTTGTCTATCTATAGTCCCAAGTGAA

WI-2625	98	G A	GGCAGTCTCGGCTAGTGGTAGACAGCACTGAAGGATGGAGGAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAAACAAGGCTATTAGGAGAGCAAAATTGATGATACTCCCTGAGGACTCGCAG AAATTACAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCCA GCCAGCAAAG
WI-2924	54	G A	TCTGTGTGTCATATTCCTCTTTGACTCTGACCTTCTGCTCTCTTATAGGAG/AJACCTGTGATT ACACTTAGGGCTACTGGATTAATTAGACAATC
WI-2939	72	G T	CCATTGTGAGGTTGGTGGGTCACCTTGTCATTCCTCGCAGCTCAACAAGTGGCTTGTCTCAGTGC CTTTG/TJCAAGACCTTCCCTCAACAAGAAATCTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT TTATCTGAAAAACTCAGCTGCACTGCTGATGTTATCTCGGGTATAAGCCACTCTCTG
WI-3203	99	G A	CTTGCTACCATGCTTTTACAGCATACACCTCAGTGAATCCCGTAAACCCCATTTATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGCAGAG/AJCCACACAGGCAATACTTGAAGTGAATTGGA GAATAAGATTGTTGGATGGATGAAGAGAGAGAGAGAGATGCTAAAGTGA
WI-3473	101	A G	GAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGAGATAGTTGGTATAGCCCTGTTTGA GATTGCAGAGAAGGAAGCAATTTAGCCCTAGGGA/AJGTAGAAAAATGTTGGTGACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAAA/AJGTGAGGCGCTCTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCG
WI-1796b	29	A G	ACACACTTTCTGTATGCTCTTCATCAAA/AJGTGAGGCGCTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCG
WI-1796	29	A G	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAGAAAGATGGGGTGAGT AGTCACATTAGGTAATTTCCAAATAA/C/TJAAAAATGGCTCTGAAAAATATCTCTCCCATGTCCCTGTC TAAATATAACATTTTCCC
WI-4360	93	C T	GCTGAGCTTTGTGGCAGAGCCAGGCAATTCAGCTGCCGGATTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAATCAGTCTCTGGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87	C T	GTTGTGCTGTAGCAGACACAGAGAGCA/AJGAGAGAAAAAGCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28	A G	CTTGAGTATCGTGGATTGGTATACAGAAAATGGGAGAGCTGGAATATCCCCCATATACCA AGGGCAAAATTGTATCTGTTTCTACAAATTATACAGTAGGAGACATTATGTTCCATGACAAATGGTAAT TTTTAACTGTGACAGTCTTTTAAATTGAGTGAATACCAATAAAATAATATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGGCTATAAATAGG
WI-1980b	140	C T	

WI-2015b	190 A G	TGTCAGATAGTCGCTCTACCTAGGTCGAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTACAAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACACAGACTAT GTGGAATCGTCTATTAGGGTTTGTATAAACTCTACATGGTCTTTTCCAACTGAGCATATACTT CTAATACCATAGAG
WI-754b	49 C T	GAAGGCACAGGGAGGAAGATGGCTGTCTATCCAGCCAGGAGAGAAGGCTGACATTTTATTTAGTAA TCCTATAAAGTGCAATCTTTAAATTTGTATTACTTTAGA
WI-754	22 T C	GAAGGCACAGGGAGGAAGATGGCTGTCTATCCAGCCAGGAGAGAAGGCTGACATTTTATTTAGTAA TCCTATAAAGTGCAATCTTTAAATTTGTATTACTTTAGA
WIR-1b	56 A G	AGGCAATCAGACCTACAGAAAGGAACCCCAATAAAACTCTGATGATGCTGATATCCGAGTGGCTG GAGGGTATGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56 A G	AGGCAATCAGACCTACAGAAAGGAACCCCAATAAAACTCTGATGATGCTGATATCCGAGTGGCTG GAGGGTATGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72 A G	TAATTTAAATGGGGCCCAATACACAGTACTTATCTCACAGCAATTTCTAAAGGCTAAATAAGAA GAAGTGAAGTCTAAAGTTATTAGCTCAGAGCCCTCACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGTCTGAGATAAGA
WIR-3a	69 A T	TAATTTAAATGGGGCCCAATACACAGTACTTATCTCACAGCAATTTCTAAAGGCTAAATAAGAA GAAGTGAAGTCTAAAGTTATTAGCTCAGAGCCCTCACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGTCTGAGATAAGA
WIR-4	47 T	GAGCCTTTCTAAATAAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCAGACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGOC
WIR-5a	209 C	CGGGACAGAGAGACAGAGAGAGTTCGACGCAITTCACAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACTGAGAGGATGAGAACCCAGCTGCAGCCAGAGCCCTGTGTCCTCCACTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5f	196 C	CGGGACAGAGAGACAGAGAGAGTTCGACGCAITTCACAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACTGAGAGGATGAGAACCCAGCTGCAGCCAGAGCCCTGTGTCCTCCACTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5e	194 C	CGGGACAGAGAGACAGAGAGAGTTCGACGCAITTCACAGAGGTTATTAGGACTCAGTCTGCTG TGAGNCATCCACTGAGAGGATGAGAACCCAGCTGCAGCCAGAGCCCTGTGTCCTCCACTGTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGACACAGACAGACAGAGAGAGTTCTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTGAAGGGGAAGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTACGTCACAG
WIR-5c	177 C	---	---	CGGACACAGACAGACAGAGAGTTCTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTGAAGGGGAAGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTACGTCACAG
WIR-5b	159 A	---	---	CGGACACAGACAGACAGAGAGTTCTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTGAAGGGGAAGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACACAGG TTTACGTCACAG
WIR-5a	37 A G	---	---	CGGACACAGACAGACAGAGAGTTCTCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGGAAGGTTAAAAAAGACACAGAGAGTCCGGTGGCTCTATGGAACACAC AGGTTTACGTCACAG
WIR-6	63 A C	---	---	TAACCCCTGAACCTTTGTCTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[AGC] CGCAGTCTGGGGTTGGGCGAG
WIR-7	12 C T	---	---	TTCTGTGACTATTTC/TAAGCATCTGTAGAATTATGAATACATAGICTTGAGATTGATC GGCGTCTATGACTATCTCTGGTCACTTGAATTGACTAATGATCTCTGCTGGCCCTTG
WIR-8	46 C T	---	---	AAACAGAAAATAGAGGTTAAGGATGGAACCTAAAGTTGTGAGAAGAGGTTATGA/C/GCTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACTAATTTGGGAACACACTGGAAACCATGGCTTGATTACT GACAAC
WIR-2	56 C G	---	---	TGTCCTTGCTATGCTGCTCTTTCCGTTGGCAGGATGATGCTGCTATTATTTCACAAGAAAGTA GCTTCAGAGGGTAACCTAACAGAGTGA/TCAGATCTATCTGTCAATCCCAAGCTTTTACATAAAA TAAGAGATCTTTAGTGCACCCAGTGAAGTGAACATTAGCAGATCTTTAACACAGCCGTGTTCAAAT GTACAGTGGTCTCTTTTCAAGTTGGACTTCTAGACTCACTGTTCTCACTC
WI-7069	93 G A	---	---	GGTCAATTCCTTTTATCTGTACGGCAGCCAGCTCTGACTTATCTCTCTGTTCTGTCATCTCTCCC CCACATACCAACTCTCTCACCATGATGATTATACCAATAATACAGTTCCTTATATAGGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A T	---	---	CACACTGTTACACCTATATTTCAAGTTTGGAAATGCA/GJATTTTGAAGCAGCAATACAAAAGTA TTTATGAAGAAATGCAATAATCTCTGAAATTAATGAAGCAATCCCT
WI-18612	37 A G TGC	CCATATTTC AGTTTGGAAA	TTGATTGCTG CTTGCAAT	

WI-18517	87	C T	CAGGAATCAG GTGCAACA	GTGTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGAGCTGTGGCAGCTTGCCAAACACACTGACTGC
WI-18668	76	C T	GGGAAAAC TAGGCAAAA GCTGCTCACTCT AGCATCTGGA	GCTAAATTAAA CTGCACTTTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTAAAGTCCAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAA[CT]AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTTCCTCTCTACT
WI-18680	75	T C A	GCATCTGGA	CCTCTGAATA TACAACGGAGC	TAAACATACAGTACTGTACAGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[CT]GCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGGTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGCTGTACCCAGGCTTTCTGTGGGAGCACACACCAAGGCGAGTTGGCTTGAAGGAGCC CTTGAGGAAACAGGGGTTCTCCGAGGGGTAG[CT]CCAGCAGGGCTTACAGCTTAAAGTCG
WI-18673	29	A G	TGTGGGCAACCTTTGTTTAAATGCAACAGTACTTAAATTTACAGCACATTCATTAATGAACCAAC AGGAGATTGCTGACTTTGTAAACATATGAATATATAATAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAAGGAAG
WI-18640	121	T C	GTGCGGGTG GGG	GCAATACCAAC TGAAGAGGAC A	ACCAGTCATGTTTTTATTTGGAGGTTAATTCCTATTAGGATATGAAGGATTCAGCAACGATTGAGATT GTGTCCTCACGGAGGGCTCGGGCCAAAGTCTGTGGGTGGGGGTGCAGAGTCTGTGCTCTTC AGTGTATTTCGGGAGCC
WI-18533b	91	T C	GGGGAGGAGGAGTGAATTCGCAAAATGAGGCAATTTTTTAAACTCCCGAGATTTCCTTTATT TATATTTCATTTTTCATCCTAA[CT]TACTGAAGCAATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	GGGGAGGAGGAGTGAATTCGCAAAATGAGGCAATTTTTTAAACTCCCGAGATTTCCTTTATT TTTATATTTCATTTTTCATCCTAAATTTACTGAAGCAATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TCATCTGATAC CTGTTTCAGAT TTC	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGCATGAGGAGCTTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTCTATCTGATA CCTGTTTCAGATTTCAGAAATAGTTGTAGCCCTTATCTCTGGTTTACAGATGTGAAACTTT CAGGACTTGTGTGAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCATCTGGGCCCCAGAGAG AGCTGCCGCCAGTGCATCATATAGGGGGTCTTTCTTCTAGTACTAGTCCCTTAAATGCCAGCTG AGTACCTGAAGGAATCTGGGAAT[CT]GCCCCCTGGCTGAAAGTGGCCCCATCATACCCCACTGTT CT
D49493	159	A T	CCTGAAGGAA TCTGGGAAT	ACTTTCAGGCC AGGCC	TATTCATAGAGGAGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAAAATTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT[CT]CTCATCCATACCACCACCTGCTGATTG
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCG	GCAGTGGTGT ATGGATGA	TATTGGCTCACTTGTGAGGCTG[CT]GAAAGCTTAAGATTGAGGTTCCACATCTGTGAGGGCTTC CTGTTGAGTGCATACCTGTTGGGAAGTCACTATGTGGCAAGAGAGGGGCTACAGAGCAAGGAA
EST10052 2	24	G A	GAGGCTG TC	TGTTGAACCTC AATCTTAGACT TC	CTGTTGAGTGCATACCTGTTGGGAAGTCACTATGTGGCAAGAGAGGGGCTACAGAGCAAGGAA

EST12502 2	52 C G	ATAACTAGGAGAGAAACCAAACTGGAGGCAAGTCCACAGGTACACATTTGCA/C/G/CAGCAAGTAT AAACAAAGTGGTTTCGATGAAGAGAGAAATGCTACGGGGAAATGAACCATTTTAAAGGGCCATGTG GTCTCGAGGCGATGAGG
EST12619 8	105 T C	CCAGAGAGAAATTTAGAAATGTATCGGTAAAGAAATAGGAATGCAATTTCAACTCACTGTACACAAA CAGGTGTTTATATCCCAATGACAGTGTTCCTGAGAT/C/GATGCAATGTGGCAGACGAG TTTCTCTCTCTTCATTATTCATTGTTCAAAACACTGTCTAGTACCAACATTTGCCACCGGCA /G/TTGAGAAACAATATGAAGAGAGAGTCACTGCCCTCTGGAAAAATCAGAGTATTTGA
EST12620 0	67 A G	TTGGGTTCTCCAGGATTCCAG/C/ACTCGTAGCTGATGCGATGAGGTCTCATCATGCTCCACGG GTCTGGGAGTGACCGGAGTGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCACTGGG TCTCAGCTTCCACTGACCTGCAT/C/CAACAGCCAGTTATTTACCAGAAATTTGTTGGGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACTGTTTG
EST12817 9a	22 C A	AGGATTTTCATGAGGCTTTAATCATAACCTAATAATCTGTTAAAAACAACAC/AGTCTGTCACTTG CAGACCCACAGGACACACATCTCTCTCTCATAGACTCTGAGGTAGGAGGTACACTGCGT AAGGAATAA
EST12941 8	23 T A	ATTTTGTGTTTCTAAATGAAGCATAATAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAACCTCCCTAAATCAGTCTCTAGGGCCACA/C/TTGGAGCAGAAAGCAGCTTCCCACCCAAAG CACCTCTGAAT
EST12949 2a	52 A G TGTGTCCTGT GGTCTC	TGCTGTCTGCATCAGTCTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCA/C/
EST13067 4	104 C T	/G/ATTTAAAGTTTACAAATTTGAGAAGCTGACACGTGTCCTACAGACACCTCATTTTACTGTGC TTTACTG
EST13117 8	66 A G	TCTGCTTTTAAAGATCTTCATAGCTGCTTGGTTTGTCTTC/C/TTAGCATATTCAGCTATAATCA CCTACATCCCTCCACAAATATTTCTGTGTGCGCAGGCGCAGTCTCCTCACTGCCCCATGATAGCC AGTCTTATTTCCACTCT
EST13121 6	44 C T	AACCTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAAATAGTCT GGCCATTT/GGACTAACCAAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAACATG
EST13226 6	74 T G	GCATCATCAGGCGCTTTTACTGAACCTTTACAACTTCCGCTCAATATGCAGCTCAGATGTGAGAG ACG/C/ATCTCTGTACAGGCGGCTACTGCTTCAATCTTTGCATGCGAGGTGTTTACACAGGCA AACAGTTTACTCCACAT
EST13230 6	GCTCAGATGTG ACAGAGA ACAAGAGGGTT	AAAGATATAAAACAACCTCCATCAGTAGCAATACAAAGTTATACATTTTAAACAGATTTTTCAGG CCTT/C/TTTGGATACCTTTAGTAGTTAACTCTCTTTTGCAACCCCTCTTGATATAACCA
EST13236 9a	70 T C TCTCAGGCGCT G	

EST13278 2a	51 A G G	CTTACCCGAA CAATAATTTAG	CATATCTTGG GTGGTGAGAA	TTGCGAGAAGCTTTTACAAGCTCCAAACCTTTACCGGAACAATATTTTAGGAGJATTTGAATATAT TTCTGTAGTTCTCACCACCCCAAGAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTC AGTCCAGA	GATGGAAAAT TGAGGAAAGGT	GCTCAGTAGATGAGCAATTGACCAAAATATTTAGATAATACCTGTTGGGAAAGTCTGAAATTTACTAGCC TGCTCTGAGAATCCACACATTTTCAGTCCAAAGAJTAACTTCTCTCAAATTTTCCATCTCCCATCAGA
EST13290 9	39 A G C T T	CAATTTTAGA AGTTGGGTT	AAATCACTTCA TGGAAAATTTCA	AGCTCATCTGCAAGCAATTTTGTAGAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTCTGTGCTTAACCTTCACTTACTTAAAGACCTAAAGACAAAGAGGTGATACATCACATATTTTGT
EST13518 2	45 C G	ATGTTCTCTCGAGTCTGTCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG GAAACATCTCCAGTAGATTGAGTTAAATGATTGAGCAATTA[G/C]JACTTTAAATAATACCTCA
EST13522 8a	66 A G	CAGTTTGGTGAATCTCAACTAGGAGCTATTTTGGCCCCCATCCGCCACCGGAGTCTCTGGAGACJAV GTTTTTGAATGTCACAACTGCGAGAGTGGTCTACTTGGAACTACTGGGTAGAGGCCA
EST13568 6	69 T C	CITTAAGGAAAGTGAGCCAGATGAATCCAAATGACCAACCTGGTTGAGAGCCATTTGGTCTAGGAGTAGA AAJTCJGCACACAAGGAATAAGGGAGAAGGAGTTCCGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA
EST13785 0	101 C G	TTTCAAGCTAAGTAAATGTT AAGATTACGGGACCATAAGAACTGCCCCCGACCATACACACACAATTTTATAGCAGGTAAACCAA
EST14038 1	25 A G	CTGAAAGGAACAAGTAATGACTTTCTTGAACAACJGJTGATTACGAAAGTGAAGGGCTACAGGG TGATTACTA
EST14083 7	23 A G	CCTCAACCATCTGTAAACCCGAGCCJAGJGAGTGACCGGGACTTGTCTGCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCACTCAGCAGGTG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAAGA	CAATGGTGCCATGTGAACATATJGJACCTATTCATAAAGTTAAATAATCCCTCTTGTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCACTGTCTGCTAAATGACCCGAACAGGAGGTAGGAGG
EST14812 2	50 A G A T A	CAAGTCAGCTT CTACATCTGGA	TAAAGATTAC TAAATCCCAT TATGTA	AATATCAATGCAATCTTGTGGCATGCTAGACAGAGGCAATATTCJTTTTGAAGATCTTTTAAAAAT ATTTGACTTGTCCCCCTTCACACTCATTTTAAATGTG
EST14815 3	128 A T A T A C T G G T T	CATCACCCAC CGGGAACA	CGGGAACA GTACCGGAA	TTTCAATGAACTTTAGAAAGTCCCGGAGTTTGCCTTTTCTAACATTTTCATATCAGGTGAACAAAT TTTGTCTCGGCAATACATAGTGGCAATGCGAGGTGAGTGGCGCGTCTCCCACTGAACCAAGTAAT TCACACAGACAAATGGCGCAACCACTTAAATAAAGTTGCCCGTCATACCCCACTATGTTTCTCC

EST15420 6	109 C A ...	GAAGAGACAA AGACAACAGA GGG	GAATAGCTGA AACAGAGATA TTATCTC	...	TTTAAACCCAGCACTGTAGATGTCAGGACTCCGATCATTTCTGCGCTATAGCTTGGATACTTA ATCTCTCCCTTTGTGATCATATATCATATAGCCAAGGGACTCAJGGAATTTTGGCTGCTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	GGTTTGGCCAT CTATAA	GATAGTTGATG TTCATTATTC CTATAA	...	GTCACCCAGCACTTTTATTAGACGTGAAAAGACAAAGACACAGAGGAG/CJAGCAGAGAATAATA TCTCTGTTTCACTATCCAGGATGTTATGCCAATATCCAGAGTCCCTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	GGTTTGGCCAT CTATAA	GATAGTTGATG TTCATTATTC CTATAA	...	AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC/GAJTTATAG GGAATAATGAACATCACTTACCTACAGCTAAACCTAATGAAGACCAATTTGCCCTCAAGGT
WI-16782	96 C T CACTGTAAGG TC	GGTGGAGTCT CTGTTCTCTCA	CTCTATCTTT CTGTTCTCTCA	...	CTCTCTCTCTCTAGACGTGGAATACACACGATACAGTATCTGGAGATGTAGCAGCTGCTCTGAC CATAATGGTGGGAGTCTCACTGTAAAGG/CJTGATGGAGGACAGAAAGATAGAAAGTTTGGGGT GCTGATGAATTTGTGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTACCTGA	CTGCTGGTTC AATCCTTATTA	G	AAAAATGTAACCTTAGAGGTTGCTCTTTTGTGTCACTTTCTGAGATGCTTTTACCTGAG/GJ CTATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C	CAGGACTTAAGGTCTTTTGGCTGGAAGACTTTAACTAAAGGTCAAGGCAACATAGGAT/CJGTGA CAGCACCACTCGGACCAAGGAGTGTGAAATCGTCACTAGGTGCCCCCCTTTTCTCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89 G C	GGTTTGAAGCAGCTTTATCTCCACTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGAGCC TTTTCCAGAAAGGCCGCTGCGGGTTTCTGAACCTCTATGGCAATTTTGAAT
EST16089 9	96 C T	CGTCTGAAGTTTCTTTTATCAAGTCACTAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC/TJAAAGAGCCATCCCTGCCCCCTTTCTTGTCT
EST16100 1	24 C G	ATCCAGCTGTGAAGGGGACAGGAG/CJGJGTAACACAGTCCATTTTAAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTTGTTTCACTCGTCCATGCTGCTGATGTTTCATAGTAAAAAGTC ACTCCAGACAGTTGGCTC
EST16104 9a	83 A G	TTCTTTTAAATAACCCACACACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGAATTTGCAG CTGGTTCTCCAGGAG/GJTTGGCCCGAAGCTGGCTGAGTTCACTCCAGGACCTCACTC
EST16118 0b	119 T C	ATGGTATAACAAATCAGTTCAGGTTTTTTT/CJGTGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCTAAACAACTAAACACACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G	ATGGTATAACAAATCAGTTCAGGTTTTTTT/CJGTGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCTAAACAACTAAACACACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ...	AGCCAAITTCACGAACCTCTATCAAAACACACAAAGGCCCTAGAGGAGAGATTACCTAATGAACGTT AAATAATTCAGGCAATTTTGTATCTAAAGCATTTTGTCTAGCTCTACAAGGCATGAATGAGGTTGT GGTCACGTTTTTGTATAGGA
EST16182 6	54 G A ...	CATTGGTGGTAGGGAAGATAGTAGTGTGCAAAATAAAATGGTAAACACGACAG/GA/AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAATTTTATTTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59 A G ...	GCAGGTTAAACTGTGGTTCACAACGATTTGTTCTTTCATAAAGAAAGAAATATCTAGTTG/G/GTAG AGGAAGGCATGTCTGCTGGCCCTTCTCGTTCATATTTTATGTCTACTGTCCCTAACGTTGGGCCGTGT GCAAGAGAGACTTTTGAGA
EST16198 4a	28 G A ...	AATCTTAGGCTCTTGGCTTTCAAAATCA/GA/ATACAGACAGATAAGAGCTTTAAGTATTTCGCATTT CCCCAGAGGAAAGTCAGCATCAATAACCACATGGGTACATGCTCACGCACATGGTGTGTC
EST16229 2c	52 T C ...	TGTGAACCTCGAATTCGCTGTCTCAAGTCTTGAGTCACAGTTTCAATTGGGAGT/GCCTCTGTGACGCC CTTGCCAGTTTCCACGAGGACGAGGATACCTCAGCTAGCTAGCTGATTCAGAGGAGGAGGCTGCA
EST16229 2b	45 T C ...	TGTGAACCTCGAATTCGCTGTCTCAAGTCTTGAGTCACAGTTTCAATT/GTGGGAGTCCCTGTGACGCC CTTGCCAGTTTCCACGAGGACGAGGATACCTCAGCTAGCTAGCTGATTCAGAGGAGGAGGCTGCA CAGACTTTTCCTCACACCTCAITGGCTGGAACTGGGTGCACATGCACATCCTTGAACATCATTTGGCAA AGGGAATAGGTCATCAAAATGCTTAAGSCCAAGCAGGAGCCATTGTTGGGGTTANAGJACTGTCC TGAACAAAATCTAGGCTC
WI-16816	124 A G TGGGGTA	GGAGCCATTGTT GTTCCAGGACAG
EST16269 5b	49 G A ...	GGCAGCTCTCTGTGGCTTGTCTGTCCAGCTGCTGTCCAGTGCACAGATGGCTAGACCTCATG CAGAACTATTGAGCAACTCTGTGGTGTCTGTCCACTCTCTTCTTCTCCGCCCTGGGGCTACCACC TCTCTCTCTCAATC
WI-16824b	83 G A ...	GTCACCCCAGCCAAATGCTTCAGGAATAATGATGGTGTGCTGACGCTGTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG/GA/CTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGGTGTGGA GCCTTCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	GTCACCCCAGCCAAATGCTTCAGGAATAATGATGGTGTGCTGACGCTGTGTTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ...	TTGCTTTTATTAATCCAGAACGGCATGCTACAGATAGTGTACAGCATGAACATTTTATTATTACAAA AATGGCTTCCAAACCAATTAATAATGAAC/TTC/GGGAATAAGAGCATAAACCGGAACAGTAACATCA
WI-16857	47 G A A	TATAATCCATCCTCCAACACACACACAAATAAGCAGCTAAATGGCAAT/GA/CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAAATGTTTTCCTGTATAATGTGGAGAAATCTGCTCTTTATGTA

WI-17010	23	T C	TTCACAGGA	AATAACGGT	ATGTTTCAACAGGAAAGCCATGTCJATGACATTCAAAACCGGTATTATTAGAAGCTCATTTAAT
EST17127			CAAGCCATG	GTITTTGAATGT	TGTTTAATGCAGACAAAATCAAGGCTAACTAAAAGCAGATCCAATGACCCAGTGATCAACCTAGA
9b	74	C T	CACTGGCAC	GGGAGGGCAGG	GGTTCACG
			AGACAGAGT	GGTG	CAGAGTCJTTGGGAGCCATGGGGCACCCCTGCCCTCCCAAGGCTTCCTAAGTAACAACCT
			AATTCCTTAT	GGACTATGGCT	CACGGGTTCATAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
			CATCTCAAGCC	TATTCAGTGAT	GAGAATTCCTCTATCATCTCAAGCCAGTCJCATCACTGAATAAGCCATAGTCCCACTGCTCTTTTCC
WI-17040	94	T C A		G	AAATCTTTCTCATATTGT
			GCCAGGGAT		TTGTTTGTGTTGTTTCTCTCTCTGCCAAGGGATTACGTATAGGTCJTTCTTAAACAAGGGGATC
			TAACGTATAG	GGGGATCCCT	CCCCACTTATAGCTGACAGCAGCAGCTGCCAACCACTGACTCTCTCTGCAGAAATGGCAGGAATCGAAT
WI-17044	47	G T G		TGTTTAAGA	CAAAAGAAAGCAAGTG
			TGGACTTGTCA		GCATGTGTTGGAGCAGATCTCCATGTAGTAAAGCCAAAGTGAGCTTGTACGCCCTAAACTACTCT/AJG
WI-17021	62	T A A C T	GCCTATACT	TGTAGAGTTAG	CAGCTGCCACTAATCTCTACAGGCACAGTAACACTTTATACAGGACACATGCCAAAGTGCCCTGG
			ACTC	TGGCAGCTGC	GAGGTGCCAATAAAATCAA
			CCAGAAAGGA		TGTAAAAATGTAGACATGGGGGAAAAAACATTCGTAATCAACATGTGCTGTTTCTACTTCCGGTA
WI-17065	90	T C C T T	AAAGCATAAA	CCCAAGAGAC	CCAGAAAGGAAAGCAATAAATTTTCJAGGATTCATTGTCTCTTGGGT
			CTT	AATGAAATCCT	
			TGTACAGCCA	GAGATGTTGAA	TTCATAAGGTTGTACAGCCCAACATCACTGTTTTCJATTCAGAACATTTTCAACATCTCAAAAAGA
WI-17066	32	A C T	ACATCACTGTT	AATGTTCTGGA	AACTCTGCACCCATTAGCAGTCATTCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
				A	
					TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAAGCAT
WI-17074	86	T G ---		...	AACTCTCTACACAGGCCCTTTCJATACATAGGAGTATAATTTGGCCAAAGACTCACACTAGAAAGTGATT
WI-1704b	108	T C ---		...	CAGATGAAACTCATGTGGCTCATGTGCAAGCTTCCCTGTGATGCTTGGAGCTTCCCACTTCCCACTTCCA
					AATCAGAAAGCAGTCAGTGGCCCGCTGGTTCCAGACGGCTTCJCTCTCTTTGTTAAGAAATTA
WI-17114a	37	T C	TTTCCATCAAG	TTGTAATTAA	AGCGTCCAAACAGATGTTCCATCAAGGACTTGTGTTTTCJGTCTCTTCACTCTGCTGTTTATAATAC
			GACTTTGTTT	ATAGCAGAGTG	AGCTACTTCCCAAGGCCAGATGCTCTAAGTCTAAAGAAGACTGCAGGCCACAATCAGAGTTACAT
			GATGAATTC	AAGAGAC	GGGA
			AGATAGTCTTC	TTCTCAGATC	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC
WI-17150	76	T G C T C T T		CTGGAAGATAT	TTCTCTTTTG/CATATCTTCCAGGATCTGAGAAAGGGCTCTCTTGTCTGCTCTTAATTT
			CATTCTTTGT	G	GAAATCGAATACGTCCATTTCTTTGTAATAAACAATAACGTTTGAAGGGCAAAAGCAAGATTCTG
			AAAAAACAAC	CAGAATCTGC	TAAACCAACATTGGAAAAGGGGACAGAGGGGACAGAGGGGAGGGGAGGGGAGGTTTTCACAGGTTT
WI-17163	43	A/G TAACGTT		TTTTGCCCTT	CTCCACATCTGCAGACAAA

WI-17178	127 T C	GGACTCCCTCA TGAGGACC	CCCTCAATTTT CAACTGCTTC	AGCAATGTCCCTCCAAATTCATTAGTATGATGAGGATTCAGTTTCATTCAGAGGCAATTCATGG GGGAGGGGGTTTAAATCCTGATGGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGCTC/JAGAA GCAGTTGAAATTCAGGG
WI-17180b	81 C G	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACITCCCAAGTCTGTCGCACAG GCTTCAACAAATTAAC/JAACAATCTTGCCCATTTTGTTCATTATCCGCAACCCACACTGACACAGATGAG GGAGTC
WI-17180a	47 T C	CACAAAAATA TAGAGAATCC TGCA	TGCGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACITTCJCCCAAGTCTGTCGCA CAGGCTTCAACAAATTAACCAACATCTTGCCCATTTTGTTCATTATCCGCAACCCACACTGACACAGATGAG GGAGTC
WI-17156	54 G C	TGTTCTCTAAA CITTAGATATC TCCA	CAAGAAATAT ATATTTGATTG TGTGGAA	TGAGGTAGCAGGGCATCTTAAGAAATGTTCTCTAAACITTTAGATATCTCCCATG/JCTTCCACAGA ATCAAAATATATATTTCTGGTTGGAAATTTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT TAATATCTTG
WI-17149b	79 T C	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGACGTGCGTGGAA ACCCAAATGTGATGCTGTATGAACACAAAGGATGGGGAAGAAACACATTTCTCACA
WI-17149a	48 C G	CAAGGTTTGA AGGAGGAACA	CCACGACGCTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATG/JCTATGACGTGCGTG GAAACCAATTTGTCATGTGTATGAACTACAAAGGATGGGGAAGAAACACATTTCTCACA
WI-17197	67 G A	GCAGAAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTTGCTATGTGCTGGCTGGACTCCAGCAATCTCCTGCCTCAGCAAGAGTAGCTGGGGCTACQ /JGGTATGCACCACTCACCCTGCTTATCAGTTTCGTTTAAATAGAAATTTTGACTTTTAGATGCGCA
WI-17198	38 A C	TCCCTCTGTC CCTAGTTT	TCCATTTGTC ACTGAGAAAT	TGATTTTCAGTACTTTCTCCCTGTCCTAGTTTTCJTAATTTCTCAGTGGAACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAAATGCACATCC TTC
EST18753	27 C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCTGA	TCGCTATGCTACCCAGGCTGGTCTCATCTTCAGGGCTCATGCGATCCCTGCCTCTGACGTGGCTGG GATAAGACACAACCTGCCACCAGGCTGCCCTAGGAGTAGTCTTAAATGCTGATGGTGGG
WI-17108b	74 C T	CCCATTCAGTC TCAAAGTAAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTAAACATACACAGATGACCTGGTTTTTACATCTCTGTTGCCATTTCAGTCTCAAAGT AAACAC/JTGGGAGCATATGATAATCGTAGTTTAAAGGAAGCCATGACACTTACAGAGT
EST19067	41 A G	ACACAAAAATTTACCATCTGACCATTTAAGGGTATAGTTTCA/JAGJGTGGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCATCCCATTCATCCATCCATCCGTT
EST19067	40 A C	CGTGACCATTT AAGGGTATAG TTC	AAAAGTTGAA TGTACTTAATG CCA	ACACAAAAATTTACCATCTGACCATTTAAGGGTATAGTTTCA/JAGJGTGGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCATCCCATTCATCCATCCATCCGTT
EST19125	28 A G	CTGTTTCTCAGAGATGACATGCGCAAC/JGTCACAGATTGTCATACAATACAGATTATGATTGGC TATTCACAATTTACAGTAGTGTCTTCTCTGAAAAA

EST20824 8	115 T G	AGTGGGAGT GCTGATTG	AAGATTTTATC TTGGACCGA	GTGTGAAGCGGAGTTTATTATTATTCAATCAGTCTCTGTAAACTCAGGATTTGAGGTTTTTA AGGATAACTTGGTGGTAGAGGGCCAGTAAGTCGGAGTGCTGATTGTTGTCGGGTCCAGATAAA ATCTAGG
WI-17347	50 A G	ATCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGTACATCTCTCAGAACTTCTCAGCCTTGGTGTAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAACTGGAGACGGGATGTGAGTGGGAACA
EST1904 b	128 GA	TTTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTC AGAAAGCAT	TGATTGTGGGTCTGGAGCAGGTGGCAGTTTCTAGGAGCAGAGGAAAGTAGACGAGTAGAAAT GAGACTGGAATCAATAGAACAGAAATGTACTAGGCTTTCTATATGGCCATTTTATAAGTG[G/A]TA TGCTTCTGAACACCTGCC
EST22111 3	82 T C	GAAGATCTGT CTGGCATCTT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT CTGTCTGGCAATCTTTTGTGGGGCTGTTTCCAAAGGCACA
EST22197 2	78 T C	AATTATCTGC TATTCTGCCA	ACCATGAAGG ATGGGT	GTTTAATGATCAGTACCAAAATCCACAGAGAACTTTAAATGTTTACAAGCAACCAATTTCTGCT ATCTCTGCCATTCACCCGATCTTCATGTGTAGAGTATCACAAAGTAAAGTTTCTGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C			TTTTCCATGGATTAGATCATCTTTTATGAGTTATAATATACATAAAATCCACCCTGTAAACAG TAGCATCAATGGTTTCTACTCTATTCJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G			TTTTCCATGGATTAGATCATCTTTTATGAGTTATAATATTCATAAAATCCACCCTGTAAACAG CAGTAGCAATCAATGGTTTCTACTCTATTCJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT CAGATTATAA	TTGAATGCTAC TGTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATGAGTTATAATATTCATAAAATCCACCCTGTAAACAG CAGTAGCAATCAATGGTTTCTACTCTATTCJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C			TGGAGGAGCTCTGAGGAGG[C]CACCAGGGGAGGTGTGCCAGGCCACCGTCGAGGCAAGTGTG GTCCAACTCTCTCCCTTTACAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTAACTGT
EST22433 c	103 A G A	AAGACATGTT CACCAAGTGA	CAGCTCAGCT TAACTGACAGA	GATGTTAATGACTTCTCTTTGAGATATGATGGAAAAATATCCAGGTACACATGGAAGACATGTT CACCAAGTGAACCAATCTAACCAAGAGCTTTACCG[C]GTCTGAGTTAAGCTGAAGCTGAATTT CTGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACAT	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAAGAAAAAATGACTTAAAAAATACAAATTTCTATCCAGAAATGATCCTTTATCTG CAC[A/G]CCATTGAAGAAAAAATTTATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCCC	TGCTGTAA TTTGACTGTAA TG	GCCTTTATGTCTCTTTTAAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTACCCCA ATT/C/CATTACAGTCAAAATTACAGGCAATATAATAGTCTAACAGAAATGCTTGCAITTT TTATTTCTCAGCTTACCATTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAATCTTTGCCTTTTATGTTTGTACAGTTTGTGTCTTCT
EST23021 0	108 T A
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAAATAGT AATACT	ACAGAAATTTTAAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAA/C/GJAATATTAG TAGTTACTATTAACTTTAGGCAAAAGCCATTCTTTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CTTTCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAGAGAGAAATATACCAGATACTTTTGTCTACTCTCCCA AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG/C/JC/TTACAGGAGGGAAGGACGCTGAGGC CAAGAGTCTGGCTCACTG
EST23733 9	31 T G TT	GGCTGTTAGTT TTGTTTTGTT	TGCACITTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTTTTTGTGTTTTTCTTTT/GTATTGATGGGATTAAAGTGCATATAACTGAAG GCAAGTCCCAAGGCCCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGCGGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCGGTCCCG CCAG	CCAGTGACGAG GCGGA	CTGACACGTCCTGTGTGGGGGGTGTCCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGGGTCC GTCCGCCAGCCCTTATG/TGCGGCTCGTCACTGGCCTTGTCACCTTTGTATTTCTGTCTGGTTGGAAA TACATCAGCCTTCC
WI-17519	55 T C A	GTTGCTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAAAGAAATCTCACTACTGCAAAATGCATTTGTCTAGCTAATGAATGAAT/C/JAGAGATTG CCTGCAAAATAAATTTAGATCTATTTTAAAGACCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95 C G	TCCTTGATACAGGTAACCACTTTTGTAACTATTTCAGAACTTCACCTGTATCTCAAGTTTTTAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	TCCTTGATACAGGTAACCACTTTTGTAACTATTTCAGAACTTCACCTGTATCTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCACTTTTGTATAATGATAGAACCCAA/C/JTJAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGATATAA	CGTCAATGTAA ATTGCGCCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCACTTTTGTATAATGATAGAACCCAAATTTAGAGAACCCAACTAGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCTTGTG TAAACACTCC	CAATCTATAG CTAGAAATCGA CAATAT	GTGTGCTGTAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCGCTACT TCCTTGTGTAAACACTCCCA/GJATATTGTCTGATTTCTAGCTATAAGAAATGGGCGCACTAAGTGGGTG

WI-17623	46 T C	TGTGTTTAAATTTAAATTTCCCATATAATTAATGGTGGGCACATTTTCGCATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAAATCTTTTGCCTGACITTTGGAGTTTTTTGGT
EST26419 1b	46 T C	ATTTACACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGATTC/GGGCAGTCCAAACTTCT TGGGAGGAGTAAATTTTCATGTGTAATGTCATGATGGCTGTTGAGGAGAAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	ATACAAAGGC AACTATGTGC	CAAGAAGTTTG GACTGCC	ATTTACACAGAGATACAAAGGCAACTATGTGCAGTC/AACAATCTGTATGGGCAAGTCCAAACTTCT TGGGAGGAGTAAATTTTCATGTGTAATGTCATGATGGCTGTTGAGGAGAAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780	35 C A A G	...	TCAGCTTTAATTTAAGGGACATGTAAATAAAAGATGTCATTTGACAGGACAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAAGTAAACAACAACCAAGAAAGCAAGTCTGTTTCCATCTTGGCTTTACCA CACTTACAACACTGATACCC
EST26900	69 G C	TACTTCAGTTTAAGGCAAAATTCACACAGAGACTGTCTC/JAGGAGACGGGCACAGAACCAGACACC GTAGAACACCAACCAATGATGAGGGGAGCAGAG
EST27152	39 A G	CAAAGGATTTTATTTTGTTCCTTAAAGTAAATCTAGAAATAGAAACCCACTGCAAGAGAGTT CTATACTAAACATTTCAATCTCTCTCTC/JTTTACATGGTGTACTCTTTTATGTACACAT CATCGGAAACACAGACTGA
EST27504 0a	101 C T ...	GCACTTTGCAA CAATTTAATA G	TTTTTGCACTTTGCACAAATTTAATTAATTTATCTG/JACATACAGTAGCATCACACCAGAGTCAAT AATGCCACTTTAGCCAAAGCTTTTCAGTATTTCTGTTACACATCTCTGTTAACAAGAACCCATACAT GGTAAATTCATTTCT
EST27662	33 G A A T T T	TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTGT/JAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAAACACACACTCTTGTTAGGAATGTTC
EST27788	51 C T C T C C A G T C T G C	...	ATTTTATAGGGGTACAAATTTCCAAAGGTGGTAAAGGGTGAAGGAAAGGCGGAGGCAATACAT TATTGAGCTGAAAACAACATTTACATTTCAAGGAC/JGJGCTTCCAGACAAGCCATGTAGAACCCAGCAT GCCITGGGACTGTGTGGAT
EST27828	100 A G ...	GTGCAGAGAGG TACTCCAAGTA C	TCTCTAAACCTTCTCTCTGTTGGATGCCAGTGACGTGGAAGTCATCAGAACCCCACTG/JGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A A C A A T C	TAAGAAGGCC TATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATCTG/JAAATG GATAAGCCTTCTTGACAAATTTCTGCCACCTCCGTTTAAAGCATCAGAACTCAATCTTATCTC TCCCGCTTCCAAAGCTTTATTTGGCAATATGCTCTATTC/JAAAGAAATGATCAATCTGTTGCCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACGCGTGTGAAGGAGACTGCTGTGTGTG TCCACCTCTTATCATAG
EST28036	37 T T C	

EST28483 7	31	T A	GGAGTAAAG GTGTTCTCT TTAAA	TTTCTCGATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTAAAT/AJATGGTATAAAATAAATCGGAGAAACATTAAAC GGAGATGTACAGACAACAGACAGACATGAGTTGTTCTGACTGTGACACATTTGGTGAAA AGAAATGGTCTAGTAATCGTTGAGGATTCGGTGATGGCCCTCCCTGTCTGJGAGACACTGCCAACCC CACAGCTGGAGGGGACCTTAAGGCACGTCATTTGTGATTAGA
WI-17724	50	T C	TGGGCTTCC TGTC	TGGGTTGGCAG TGTC	CGAGCTGGAGGGGAGAACACAGACAGAGTGAAGTGTCTATTAGTTACATCATCAAGTGTACATCTG TTT/CACATGATTATGCGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
WI-17730b	68	T C	TGAGCCTGGGGAGAGAACACAGACAGAGTGAAGTGTCTATTAGTTACATCATCAAGTGTACATCTG TTT/CACATGATTATGCGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
WI-17730a	39	A C	GACCACAGAA GTGAAGTGT CATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAGAACACAGACAGAGTGAAGTGTCTATTAGTTACATCATCAAGTGTACATCTG CTGTTACATGATTATGCGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
EST29041 5b	53	G A	GGACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTGAGAAATGTAGTTTCATGAGGAGAACACACATTAAGCATCTGTCACCT[G/A]GCTAACTCCT CAATCAACAATACCCCTTATTTTATAGCCATGAAAAC
EST29128 4	58	A G	CTTTTGAAGGACACACAGTCTTTGTTGGACTTGGCCCTACCTATTCACGAGGTGCC[A/G]TTATTT TCACTTGGTTACGCTCTGTAGAGGCCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTCTGGGGACACT
EST29912 3	103	C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGT TCATCTTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[C/T]ACAGAAAGATGAGACACTTACGCCATG GCCATGATACACAGCAGTGA
EST29936 8	121	G C	TATGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACTCTCTGACTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99	A G	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTATTTTAAATATCC[A/G]GGATTAAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16280b	86	G A	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAACCCAGA GTTTCACAAATAGGTAGTGG[A/T]AACCCAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16280a	59	G T	CAAGAAGAAA A	CTACCTATATT GTGAACCTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAAAGAA[G/T]ACCC AGAGTTTCACAATATAGGTAGCGGATAACCCAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC AAGAGAAACCGGAAATATTGCTTTCTTGG[A/G]CGCTGTTCTTATACCCCAATATCATAGAATT GTTGTGCTCTATATGTTGAGTTCAGGTTCAAAATCTTTTGTCTAATCAATCCAAATGAAATACCTGAATT TTCTCCTCTGTTTCAAAA
WI-17835	30	G A	TG	TGGGTATAGG AACAGGC	

EST31951 4	87	C T C C A A C A	GGTGTGTCAG CACTOC	CCACCAAAAT CACTOC	ACAGCATTATTATGTTTACTTGGTAATATCAGAGACTGAACATTTTCACCTCTTTTAGCAATGACA TCGGGTGTCAGCCACACATGAGGAGTGAATTTGGTGGGAATTTCTATCACAATTTCT
EST31968 8b	95	T G	CGAATTTGCTCTCTATTATTTGTTAGTAACTCTAAAGATTTGGGGGGGGTACTATAGT GCATTTTATAATGGGGATTTCTGCTTTGAACTGCCCACTGATCTTACATGGGAAGGTGCAAAAG ACAGTGGTACTGCTOC
EST31968 8a	75	T C T	GCGGTACTA TAAGTGCAAT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTATTATTTGTTAGTAACTCTAAAGATTTGGGGGGGGTACTATAGT GCATTTTTCATTAATGGGGATTTCTGCTTAACTGCCCACTGATCTTACATGGGAAGGTGCAAAAG ACAGTGGTACTGCTOC
EST32063 2	103	C T	TCATGGATGAACAGAGCTACCATGCCACATCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGTTCTGTTCCAGCCCATGAAATAGCAACCGCAC AGTCATGAGCACTCGG
WI-16303	65	A G	AAGGCTTCCAAAGCATTCAAAAGGCATTTGGGTGTTGCTCTAAGTTTCTGGTCACTGCAGCCCTGAG TTCGTGTTAGGGAGCACCCCAAGCCAGTAACAATAATGTTCTTGCAG
WI-17800	29	C G G A G A A A C T C A	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACTGAGAGACTGGGATTAATTTAGGAAATATTTCACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTT	TTGGCTTAGGT TCTACTTGATG T	AACTGTCACTCCTAAAGCTGGGATGACTTTCCTTGTGTTCTACATCAAGTAGAACCTAAGCCAAT TCAGAAATCAGAATCCCTTTTGTCCATCAATTCAGTAACCTCAAGCTGAATTAATTTGTTCTCT GTATCTGATGATGTTAACCCTGCTGCTGATGATTAATTTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAGATAATTAATTTCTTGGTTTAAATCTTGCAGCAAGCAAAATATTAJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860 4c	121	T A A G C A A A T A	TTTGCCAGCAA ACTTCTCAA ATTATAGCCT ACTTCTCAA ATTATAGCCT	ACTAAGGAGC AGTCAGTCGG CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTGTGTTTATAGCTACTTCTCAAAATTTGTTTGTGTTGATGACAAACG GGGGAATCTACAATGCTCACATCACAGTAACTACCA GAAAAAAGATCAATGTTTCCCTTTATGGGTGATGCCACCATGATTCCTCACCAAGCATGATC AATGCCACAGAGAGTGGATGCCAAAGAGTATGG GAAAAAAGTCAATGTTCCCTTTATGGGTGATGCCACCATGATTCCTCACCAAGCATGATG ATCAATGCCACAGAGAGCTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	
EST33460 1	44	G A C A	AGCGTGGTTT CAATACTAAA	CTGTATTATT GTTAAATATT GCATGTT	CTATCCAAAGATATTATTCAGCGTGGTTTCAATACIAAACAGATGTAACAATGCAAAATATT TAACAATAAATACAGTGATTAAATAGCCATGGCATATCCAGTTGATGTAATCTTTTGCAA

WI-17904	50	A G A C A C	AAAGCATGAC AATAAAATGA	CGCTTATGTTA ATAGTAATTC	CAAGTGAATATTGATACATGGTGACAAAGCATGACAATAAATGAACAC(A/G)TACGGGAATTAC TATTAAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACACAAATGA
EST34149 5	69	A G A T	TGCCAAATAC TCAAGTGTGA	AACACTAGCG AGAACAACTA ATAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGGAAAAATGTGTGCCAAATACTCAAGTGTGAA T(A/G)GATTTTATTAGTTGTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTCAGC TTACAAATCACACAAGT
EST34343 8	95	C A	GGACCATATG ATATAAAT	...	TGGGAAACATAAGTTAACTCAAGAAATATATCCAGTCTTATGTTACTAAAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC(A/T)ACAAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98	C T C C T A A A G C	GGACCATATG ATATAAAT	CAGAAATTATG TGATAATACT CCTTC	GGTACACAAATTTTAAATGGAAGGAAACACAGGTAATGTTGAAAGAACATCAGTACAGCTGGGAGACAGG GAGGGACCATATGATATATACTCTCTAAAAGC(C/T)GGAAGGAGTTATATCACATAAATTTCTGGGC GCTACAGAAAGTTTTCATCA
WI-17993	118	A C	GTAGAGCGGA AGGGAAACAG	AGGCACATGGG CAGC	CTCAGTAACTCCGGTGTATAATCGCCATTTATGATTTTATGATAAACAACCTCTCATTTGTGA AAAAACAGCTAAGGTGACATCTCCAGACCCACCACTGTCCCTGTAATG(TA/C)CTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84	A G A G G G A C A G	GTAGAGCGGA AGGGAAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCCGATGTGATGGTGAAGCAGCATGAAAACAACATCTCCCGAGGCCCTCGCAGT AGAGCGGAAGGGAACAG(A/G)GCTGCCCATGTGCCCTGCTCTAAAGACGCCACCCCTCAGGTTGATGT CACTGTGGGAGACCGGGT
WI-17136	33	C G	GTAGAGCGGA AGGGAAACAG	AGGCACATGGG CAGC	ATTCTTTTATAAAAACACCCATGTCCCTAAAATG(TC/G)ATTCACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAAAGACAGAGAAATGTGCTCT
WI-18041 EST35164 8a	24	A C	GTAGAGCGGA AGGGAAACAG	AGGCACATGGG CAGC	GCCACTGAAAAAGGTGCTCTTCC(A/C)GTTTCTAACTCCCTGGACTCCCTCATTTGGAACTGAAGTCT ACAGATGTTTCAGCTGGACTAGTTTAGACTTTTGCTGATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATCTTAATCA
WI-18052b	67	A G	GTAGAGCGGA AGGGAAACAG	AGGCACATGGG CAGC	ITGAACCAAGGCCCTAACAGATGACTACAGAGGCCCTTCAAGCAGACGCCCTGCCCC(A/G)TCTTGA GATTCAGAAATCCAGAGGTCCTGCTGCTTTAGTGGTCTTCTGTGACATTTCTCTTG AGCGAATGAAATGCTACAGGCTCCCTGAGTTCCTTTCATGTAAGAACTCTTGGTTACACATCTTAG A(G)ACAGCAGAGCTGCTCAGGAGGGTGTGTTTAAATGTCGTATGCTCAGCAGCAGTGTGCTGGC ATGCCCATCCATGCTTT
WI-18052a	50	T C A T C	GTAGAGCGGA AGGGAAACAG	AGGCACATGGG CAGC	AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTCATGTACGAATG(TC/T)GTTTACACATCTT AGAACAGCAGAGCTGCTCAGGAGGGTGTGTTTAAATGTCGTATGCTCAGCAGCAGTGTGCTGGC ATGCCCATCCATGCTTT
WI-18054	46	G A G A T A A A A	GTAGAGCGGA AGGGAAACAG	AGGCACATGGG CAGC	CTGTTGTGCTGAGAACAGAGGGGTCAAGGAGTGGGGAGTAAAG(A/G)TGGAAAGCAGGGTGAACG CATGCGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	GA	AGA	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAACCCCTGTGGGAGCTGCTAGCTGATTTTCAGAG/A/GAATGTCAC AATCATACCACTGGGAGAGAGTAAGCAGAGTGTCTTATAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T	C	GCATAAAATT TTCCAGTTGGT	CCCTCGCAACC TGCT	TTTAGCACCATTCTTAGTGAGCAGGATCTTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	A	C	AACCCACTAC TTACTCAGAGT	AAAACATAA AGAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTGTAT/CJATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATTTCTCTACTCAGAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	C	T	GTGTAT		TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCCGTG TTTGACTTTTATC/TJCTTATGTAAATGAAGCCAAATGCATGTTAATCCTCTCTCTTTGGTGTAT
WI-18080b	65	GA				TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCCGTG ATTGTTGACTTTTATCTCTTATGTAAATGAAGCCAAATGCATGTTAATCCTCTCTCTTTGGTGTAT
WI-18080a	41	T	C	GCAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAACA	TGGCATAAAGTTTGCATAATCAATATCAAACTAGTCTCTCTCTTTGTAATTAATACTACTATGCC CGTGTGACTTTTATCTCTTATGTAAATGAAGCCAAATGCATGTTAATCCTCTCTCTTTGGTGTAT GTGGGCATCCTATAAAGCAGCCATGTGTGAACCAATGATATGCACAGAAAGCATCTCTTGAJ TGCTTTGTACACGGGTTTCTTTCAAGAGGAAGATGACTAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18086	63	GA				AACTACATAGTATGGTGCTGGCTTGAATCAATGGGTAAGCCCTTTAGTGACTCTTTGGTATTCCC TTCTCTTTGGTATGAAGAGACAGACCTCTGCTGGAGGACTCATACAAATGTAAAGAAAGGGTGAG TCAGT
WI-18115b	71	C	T	TTAGTGACCT TTGGTATTCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCTGGCTTGAATCAATGGGTAAGCCCTTTAGTGACTCTTTGGTATTCCC TTCTCTTTGGTATGAAGAGACAGACCTCTGCTGGAGGACTCATACAAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70	C	T	TT		TTTTGAGAAGCAGCTCTGTAAGGCAAGGATGCATCAAAAATGGCTTTGAGGATTAATCTCTCTTTA GGTAAATTTGCA/GTAAAGAACATAAAGCATTTTAAAGTCCACTGCCGCTTAAAGAACT GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCAAGAGCCATCTTCGGAAAGCTC/GJTGAGCACAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18169	115	A	G	CCATCTTTCCG GTGCTCCA	GAGTCTGCTT GTGCTCCA	TGAAAGAAAGTGCACACAGCGGACACTG/AJTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGATGAGCTGGAGACATTAATCTCTGGCGA
WI-18190b	26	G	A			

WI-18190	62	G A ...	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT	... TTG	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAAGGATGAAGCTATCATGTGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAACTCTGGCGA GACAGTGAAACACATTGAAACACACAAATACAAACAAACATTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACCGTA TGTGTTCTTGAAAC
WI-18181	100	A C CAGATC	AGCAGAGTTC	CCCTCCCTCTCT	...	ATTATACAAAGCATTTCCTGAGTACAAACTAGGGGACAGGTATTTTCAAAAAACAATAGAGCAGA GTTCTGOCCTG/GA/GTGTGGGGGAGAGAGGGGATTTCAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAAATCCCTTC
WI-18215	78	A C TCCCTC	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT	...	CATTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/GAA CCCTGAAACCTTTATTTTGAATTTGAAGTTTTGCTCAGAACTGGCGAGAACTTTCACATTCTG AC
WI-18232	60	T A A A	GGAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT	...	TTTAAAAATGCTTAGAATTTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACAAT[C/C]CTGTCTCACTAGTCTATTCTCTGTGGGCATTTCGGCAGAAGTGGC
WI-17892	76	T C A C A	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAAACAG	...	AATATCCCAAAATGTTAATCGTAACATACT[G/A]GAAAGCTTTACAGTAGAAGTGTAGCAAAAT TGGATGCCACAACTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAATGTTTCTTGCCTATATC TGCAAAAGATCGAACAAAG
WI-18242	30	G A AATCGTAACA		CCTTC	...	GCATCAGACATCACCCTCTCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCAATC[C/T]ACATTTGAGAC CGCAACTCCGAGGTACCT
WI-18266c	119	C T	GCATCAGACATCACCCTCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCAATCCACAT[C/C]TGAGAC CGCAACTCCGAGGTACCT
WI-18266b	124	T C ...	AAATAGGAAA TATGGACTATC	TTATGCATCA TTTGTCGA	...	GCATCAGACATCACCCTCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]GCACAAATGATGCAATCCACATTTGAGAC CGCAACTCCGAGGTACCT
WI-18266a	97	C T T T C A A A	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	...	CTGAGCCTCTGGATATGGTTAGTGTCTATCATTTAATTTTGGAAAGCTGCAGCTATGTTATTTC AAATAGTTATCTTCTGCTCCCTTTTCTGCTTTTCTGGGATCTCATCTCTGCAATGTTATA AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAAACAAGAGG A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGACATAAATTTTTTGTGAT TCACA
WI-18312	73	A G A A			...	
WI-18330b	66	A G	

WI-18330a	49	GA	TCCTGTAA AATCAGGGAT	AGTCCTGACTC ACTGCTACA	TCACA	AAACATCTACAGCTGTCTTAGGCCATCTCTGTAGAAATCAGGGATAAGA(GA)CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACATAAATAAAGAACATAATTTTTTTTGTGAT
EST37564 5	85	T C	AAATCAAGC CATCTACAA	CTATGGAGGOC TCAATGAGA	TGTA	AAATAGTTAGCCATAACAGGCTGGAATTCCTGTTAGAACTACTGCATGTTATTTAAAGCTAAATTC AAGCCATCTACAAAGATTTCCTCATTAGGCTCCATAGGCTGCAAAACATCAAGGCATTAC
WI-18327	104	GA	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	GT	CAAGGGATTATTTACCTACAAAGTAAAGGAGGACAGCTGGGGCAGTTTCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTTGCTTAGGCTAGTTGAGCTGAGCCATTGTAATCGGAGGCGAGA
EST37624 6b	102	GA	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAATCCCAATACGAACAGTGCACGCTGATGG OCTGCAGTCTCTGCCGTGCTGGCTCTCTGACGCTTCAATCTACATGGCTGCTTTTGGCTCC
EST37624 6a	58	C T	TCTGACCTCCCAATTC GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAATCCCAATACGAACAGTGCACGCTGATGG TGCCCTGCAGTCTCTGCCGTGCTGGCTCTCTGACGCTTCAATCTACATGGCTGCTTTTGGCTOC
WI-18357	89	C G	CCAGCCCTTA GCATCAA	AGACTGAAGAT GA	GA	TCTGACCTCCCAATTC AATGTTTTAAAGTCTCTACCGTCTGAGGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCA TAATCCAGCCCTTAGCATCAA(C)GTCATCTTCACTCTTTCAGTCTTTCAGCTTCCAGCCAGGTCCAAAGCTT
WI-18012g	117	A G	GTGGACCCAGAGACAGCC TTTTATCTGGGTACGCTCTCTTAATGGCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATGAAGCCACTTTTGGCCCTTGGTGAAGGTGTTTCTCTGATACA
WI-18012f	113	GA	CGCTGACGTTTGGAGG TTTTATCTGGGTACGCTCTCTTAATGGCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATGAAGCCACTTTTGGCCCTTGGTGAAGGTGTTTCTCTGATACA
WI-18012e	112	C T	GCCACTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	...	CGCTGACGTTTGGAGG TTTTATCTGGGTACGCTCTCTTAATGGCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATGAAGCCACTTTTGGCCCTTGGTGAAGGTGTTTCTCTGATACA
WI-18012b	46	T C	CGCTGACGTTTGGAGG TTTTATCTGGGTACGCTCTCTTAATGGCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATGAAGCCACTTTTGGCCCTTGGTGAAGGTGTTTCTCTGATACA
EST38390 4	75	A G	GCAAAAGGA GCTCTGATG	CTGATTAATAA ACTTAA	...	CGCTGACGTTTGGAGG CATATCATGCCAGATCTACACCCAGAGTAAATCCCATGGTATGTTACATGGCAAAAGGACTC TGCAATTTGTAAGTTTATTAATCAGCTGACTTTAGCATTTGGGAGATTATCTGGAT

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CACGCACTCT GGGAAGC	TAATAAACTGACCCAAATTGGTAAACTGTGCTCTGGACTGAGAGAAACAATGAAATCTGTAAAT ACCTGATGAGGATGCCAATACTTCGT/GGCTTCCAGAGTGCAGTGATGAATCTTATAGCC
EST38519 0	24 C T T	CCTGCACTCC TAAAGATCT	TCTGTAGGAC TTGGGGA	CCTGCACTCTTAAAGATCTTTTC/TTCCCAAGTCTCTACAGATGGTATATCTCTCGAAAA AGATGAACGTCATCAATGGATTGCTGCTCTCGTTTCAGCTTTGATTTTTTTTCTCTGAGAACCTTG TCTCCCTGCTGATT
EST38575 1	66 T C A A	GAACATCCA TGTTCTGTT	AGGGAAGGA GTATAACAT	AGTGGTCAAAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTCTGTTTAA T/C/TCTCTTATGTGTTATACTACCTTCCTTTCTCTTTCTTATACACATAGATTTTCCTTAAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGC	CCATCTAGGCAGGCTACCTGAGCTCTGCTGCTCCAGAGTGGTGCCTACGCCCCGGGCCCCGTGG AGTCTCCGGGGGCCGCCCTGCTCCGCCCTTC/CGGCCAOCATCCATCTCCACAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAAC TGGG C A T T T C A A	TTGCAAAAATG AAAGGAAAA	TATAGTAGGTACTTCTCTGCTGCAGCAGGAATTAATTCAGTCTGAAC TGGGCA TTTCAAT/C/CGCGTG GTATTTTCTCTTCTTCA TTTTTCGAAGTAAAAATCAT
EST38654 5	42 T C G T T T A C A	AATGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTACATAT/CJAGATAGAAAGATTAAAGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTGGACCCAGGAGGTTGGTTCCAGCATATA GGATCCTCAGCTACCTGGGACAGCTGAGAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTCCCGAGAGCCAGCGGATGTGTGCCCTCTCTCCCAACTCATCTTTTCAGGAACACGAGG ATCTTGTCTTCTGGAA
EST38707 9	75 A G	TGCTCCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTCACTAGAGGGGAGAAATCAATCACTACCTCTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATATGG/AG/CTTAAGTCCACGATGTGACCTAACTCAGTTTAAATTTCTTGCC TAGCAGCACC
EST38759 2	86 A G G G T G A T A T G G	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATCAAA	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGT/AJTTTGAATTCAGAGCAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCTCCAAATGCCCTTTCATGAGTAGGATCTCCTAAGTGGTAC AAACAACCAACATGGTG
EST38775 1	40 T A C	TGTTATGAGA ACCATTACA	GCTGACTGGCA CATGCTTT	CACCCATATTTGACCAAGGATGAAGCTAGCCATGCTCTTTCAC TTTATGTGTTCATTCAACAAG TGTTATGAGAACCCATTACAC/CA/AAAGCATGTGCCAGTCAAGCATTTCTGTAATA
EST38815 4	91 C A C A	CACGAGTAAA AAGAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACTTCTCCAAAGTTTGGGTTTCCATATTTGTTATTTGTTATTTATTA TTCAACACGAGTAAAGAAACTCATGAC/C/TTTCTCTCTGGACTGCTCTCTCCCAATCTCGAT ACCGACTGCACTGTG
EST38858 4	98 C T T G A C	GCTGTAGAATT TGTCGATGC	GGAAGGAGGG AGGACACAG	CCCTTAATGGAATTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTGTG ATGCT/C/CTGTGCTCTCCGCTCTCCCAATGAGCACATATGACAGGGGAGGCAAGCATGCTGGA TTTGTCTTAGTTGTTAA
EST38865 2	72 T C T G T G C A T G C			

EST38878 9	47 T C ATCTAA	AAACATCAIT ACTAGCCTAG CA	CCTTCAATAAA TCTCATGTCT CA	CCAAATGAGAACCAAGTAATTAACATCATTACTAGCTAGATCCTAAATCTGTGAGGACATGAGATTT ATTGAGGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTTCC TTATTCAATGTCTATCTACACATTTCTTATTTTATTTTATTTTCTCAATTTCTCAATATCGGATTTGTC TCATGAGATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCA[GC]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 GC	TGTCATCTCAC ACATTTCTTTAT	CGATATTTGAG AAAGTGAATA CAA	TTATCAATGTCTATCTACACATTTCTTATTTTATTTTATTTTCTCACTTTCTCAATATCGGATTTG TGCTCATGAGATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAATTT TA
EST38882 6a	35 T C TTTT	GCACAGCATG GCTAATAACG	GGTATTGTTG ATTCCCATCTT T	GCACAACTAACTTTCAITTTGTGGATTGCACAGCATGGCTAAACAG[AG]TAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATCTGCTGGAGGGAATATAAATTT AACTGAATGGCAGTGAAACACTACACATCAAACTTAAAGGAAATGTGGTTAGTGTGAGTTGAG GGAACTTTATAACCTCAC[AG]CGCTTTTTCACAAACACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38909 5	47 A G	GCACAGCATG GCTAATAACG	GGTATTGTTG ATTCCCATCTT T	GCACAACTAACTTTCAITTTGTGGATTGCACAGCATGGCTAAACAG[AG]TAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATCTGCTGGAGGGAATATAAATTT AACTGAATGGCAGTGAAACACTACACATCAAACTTAAAGGAAATGTGGTTAGTGTGAGTTGAG GGAACTTTATAACCTCAC[AG]CGCTTTTTCACAAACACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G CAC	TGAATTCCTT GGTGGG	CACTGCAATCT CAOCCCC	TAAACATTCCCATTTGAATTCCTTTGGTGG[GC]GGGGGGGGTGGAGATTGCAAGTCTCAAGATAAA TATCAACAATATATCAAAACTTCAAAATTTGTCTATGCATTACACACTGACATGAGCCACAAACATT CCTTTTCACAGGACTGTAC
EST38955 5	30 G C	GGACCTTTGGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCTGGGAGATCCCGGACCTTCGGTGAC[GC]ACAGGCTCCCTGGCAGGGCTTGG CCCTGACCGGGCTCCCGAGCTCGGCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACT C
EST39002 0	42 G A	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCTTAAGTTTCCGGGTCTTCTCAGTCTGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGGAGGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGTC AAAGACCTAACTTCTGGA
EST39004 8	79 T G	TCCCTATTAT CCATGATATTT	GAATGGTTGT GAAAAATATA TTGATAT	AAAGATAATGTCAATCACACCAACATATAGAAACATATAAGAAAAATAAGATATCCACCCTAAAT CCCTATTATTCATGATATTTTCA[GC]AGCAACTAGTATATATATATATATATATATTTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C TCA	CCTTTGCTCTC AATTTTAAAC	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTTCATGATTTTCTCAATTTCTCACTTCTGAGTTTCTGGTCTTCTCAATTTTAACTT TTCCTTTTATATAGGGAAATAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCCCAAGTT TTCCTTTTATATAGGGAAATAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCCCAAGTT
WI-16403	69 T C ACT	GCCTTAATGGC TACAGAAAGA	CCAGAACCCAG ATGTGTTTAAA AA	GCCTTAATGGCTACAGAAAGAG[GC]TGGTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATATGCTATTTAGCAATAGGTGCCCTGAA
WI-16406	24 C T AGG			

EST39236 0b	57 C G G T C T	TCATCTGAGA ATAAACTTCCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGAAATAAACTTCCTGTCTAAATTTCCAA/C/GIACATATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T G G A T G C C	CCTGAAACAG GGATGOC	GCACAATTAA ACATAGTACCG AGAA	CAAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCQ/G/I TTCTCGTACTATGTTTAAATTTGTCTGAGCCAGCAACCTCGAGTTACCCGGCTTTTACCCACGGCC AGCTCTGCTGTCTGCAT
EST39366 2	72 T C			AGAAAACATTCTGCTGATCAGAGGAAAGATGATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT/CJACACTGAGAGGAAATGGAAAAGAAATGTTGCATAAAAGCTTTTCCCTGACTCTCA GAGGGTTTCA
EST39371 9	86 A G G G T G A G A G G	CATTGGATT AATTCACATTT	TGATTGAGAC AATTCACATTT	AAAAGCTGTAGCTGGCAAGTCAAGTTTATTTATGTGTGTAATTCCTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG/G/AAATGTGAATGTCTCAAATCAATGCTTCTTCTTAAAGATT GACATTGCCCAACCTGC
WI-17177	23 A G			ACAAGTGACATATCCAAACCAACQ/GJTCATCCCCACCTGTGCCCTATTCTTCTCTGTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAACTGCACGAAGGCTCCCGGTACTCTCCCTCGGAA G
EST39428 8	31 C T A T T T G A T T	GCTCCCCACA TAACTGATGTT	GGTCCCTATG AAGCCACC	AGTTCTGCTGGTTGCTCCCCACAATTTTGAATTC/JGGTGGCTTCATAAGGGACCCAGGATTCGCATT TTCTGGGTGGGGCTTAGGTAAATCTGTTCCTTTGGTCCACAGAGCAAAATTAAGAAGATCAGGTCT GGCTGTTGC
EST39430 2	45 A C C	GGCAGAGGAA TAACTGATGTT	CAGGGTCGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGCAGAGGAATAACTGATGTT/CJCAATACCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCCAAGCTCCGGTGAGGATGCTCTGGG
EST39446 7b	117 C T G A G T A A	CTACTGACAT AGGCACTCA	TCCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACACACGTCACCTTTGGAAGAAAATAACAGGAACCTATTATAT ACGTAAATCACITTCATACCTGCCCTACTGACATAGGGACTTCAGAGTAATA/C/JGGTTTATGTCAGT TTCCAGGATTTCTCC
EST39465 2	80 A G G T G G C	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAACGAACCTGAACAGAAA TGACAGAGGGTGGC/MGJAGAGGGGCCGAGATTGGGTTCAGGGCAGAGAGGTGGAGAGCAG
EST39501 0	81 A G A A C A T T A G	AAAGATTCTT GTAGACATCT	CACITTCGAATT CTGAAGGCT	TGCTTACAAACCCATAACCATAGGCCATGTGTTTCAGACATCTTGACCAAGCTAAAGATTCTCTGTAG ACATCTAACATTAG/GJTAGCCTTCAGAAITGCAAGTGCAGTTCAAGTCAACCAACCAATTC CACAATGGGGACTGCTGAAGAGTGGACAGTGGACCTTACTTTGGTGACCCCATACATTGTGGTCA CATGCTTTAGCCCATAC/CJCATGGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGGCATG GCTATGTAGACATAAAGA
WI-18387b	84 A C			

WI-18491	109	A A A A A T G G T	CGTGTGCATTT	CTAATCAGATGAATACATGGAAGGCGTTTAGCAGAGTGCCTAAACACACAGTAAGTAACCAACAAT
EST50757		AGGTGGTATT	TCITGTAATCC	GGTAGGTGGTATTAACTACTATTATTAAATCCAGAAATGAC[G]AGGATTACAAGAAAATGCACA
b		A A A A T A C T A T T	A C C C T T C A C C C	OGT
	79	G A G C T D G A G G	G D C C	AGCCCCCTCCACTCCACTCTGCTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTCTTTTATAT
		C T G C T T C T		GTG C A G G G C C [C] T T G G G G G G T G A A G G T C A G A G A
WI-17675	103	G G A C A T T T G G	G G G A A C C A C C	G A T C T T G A A A G C A C T A G A A A C T A A A C A T C T T C A C C A G G T G C T G A A G A A A A G T G T C T T C G T T T A A T
		A T G T G A C T T	C A G G	T G C C A A G C A G G A T G T G G A C A T T T G G A T G T G A C T T T C G T G G T G G T T C C C A T A G A T T C A C C A T
		A G A T A A A C T A		T G C C T C T A A T G G T G T C T A
WI-16543	67	C A T T T G G G T T	G A T T C A T C A T T	G A T C C A T T A C C T A G G T A A A A T T C C T G A A T G T C A A C A A A G A G A T A A A C T A C A T T T G G G T T T G G
		T G G	A C A G G G A C T T	G T T A G T C C C C T G T A A T G A T G A T C A A G A A T C C T C A A G T C T G C T T G C C A C C A T T T A A T A C G T A T T
		G C C A A A A A G G	T T A C T T T T G T A	T T T G T T A A G G C T G A A G T T
WI-17687	107	T T G G G A A	C C G A C C A G C A	A T C T G A G A T G G A A G A G A T T T C A T C C C A A A C C A T C C C C C T G A C C C C A G T C C A T G A A A A T T G T C
WI-		A G G C A T T T T T C	...	T T C C A C A A A A C C G G T C C C T G G T G C C A A A A A G G T T G G G A A [C] G T G C T G G T G G T A C A A A G T A A T T
17690b	79	A G C A T T T T T C	...	G
WI-		T A G C T G T G T T	C A A G A G T T A T G	A C A A C A T G T G A A A G A A G A T A T G T G T C T T A C T C A C A G T G G A G G C A T T T T C T A G C T G T T T [G] A
17690a	63	G A T A G C T G T T	G G T C C T G A A T C	G G C T T C C C T A T [G] G A T T C A G G A C C C A T A A T G T G T C T T A C T C A C A G T G G A G G C A T T T T C T A G C T G T T T [G] A
EST51717		G C G A A G A C A	T T G A G G C A A T A	T T T G G C T T C C C T A T A G A T T C A G A C C C A T A A C T C T T G T C A C A C A T C T G C T A T G C T G C T G
b		G T G A G C T G T T	A T C C A G C T C	G A T C C A A T C T C A G T G T C T A A C T A T C A T C C C A G A T T A T T C T G A A G T G G A A C C A C C C T C C G A C C C A A
EST51717	128			T G G A A C A T C A C C C A C T A C C T G G T T T T C T G G A G A G C A G C G C G A A G A C A G T G A G C T G T T [C] T G A G
a				C T G G A T T A T T G C C T C A A A
				G A T C C A A T C T C A G T G T C T A A C T A C T A C C C A G A T T A T T [C] T T G A A G T G G A A C C A C C C T C C G A C C C
				C A A T G G C A A C A T C A C C A C T A C C T G G T T T C T G G A G A G C A G C G C G A A G A C A G T A G C T G T T C G A G
	39			C T G G A T T A T T G C C T C A A A
EST53012	97	T G G T C A C T T T G	G G C T C T G C C A	T T T C C A G G T T G A C A G G T T T A T T C A C C C C T T C C A T C C C C A T G G C C A C C C A G C A G C A G G A G A C A G
		G G G G C	G G C	G T G T G C T G A G T C T G G T C A C T T T G G G G C C [C] T G G C G T G G C A G A G C C A C T G G G T T A C A T T C T C T G T
				G G G C A G S T G T G G A C A C
EST53349	96	T G T T G A A A G C	C A T C T G G A T A T	A A A C T G C A A T A T A C A A A A A C A G A A G T C C A A G A A G G C T A A A G T C T A A G C T A T A A T T A C A C A T G
		A G T C A C A A T G	C T T G T C A C A T T	A A G T A T A T T T G A A A G C A G T C A C A A T G T A C [A] G J A A A A T G T G A C A A G A T A C C A G A T G T T T A A
		G A G A C C T G C	G C C T T T C T A A	T T T C G A A A T G T C C T C C A T G A C T T G A C A G A C T G A G A G C C A G C C A G C A G C C A G A C C T G C A G A A C T
		A G A A C T A A A	C A A T A A A T G C T	T A A C A C [A] G J A G A C A T T A T T G T T A G A A A G G G C A A G T C T T A C A C T C A A A T A G T T T A A C A T G A A C
EST53389	74	A G C A	C	A C A T T A A A G G G A G A T G G C C

[illegible]

[illegible]

X57830	106 G C C T	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGAAGGCACACTGAGCAAGTTTTACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTGGTATGCCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTGAGCTGTGAG CTTC
X74070b	72 T G T G A T C	CTTTTAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATATGACTGCTTTTAAAGAAATTTTGTATTG GATCT/GGATAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTCTTATACAAATTCATCTTTCGAGCTAATTAAAGCCGAAAGCCCTGGGAATCAAGTTT GAA
Z48804	44 C T		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTCTCTCATCACAGTC/TTAAAGAGCTTCTTCCGGAAGGG CCTTTAGGATAGAGAAAGGGTTTCATGCACACAGGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTGGCCACTAGGAAGTTTTCTGAGGCTGGCTGTAAGTAAGTGAAGG TCCA
D28513b	133 A G		---	ATGACAAAAGCCACACATTAGAACTTTGGCTGCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGTGAGCACTTTGGACATGGCTCACAAGCAGTTTTTGTGACTGCATGAATGCA GTGTGCGTGCAGCATGAACCTTGTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGCTTC AGCTGTACATA
D29833b	85 A G		---	CCACTCCATCTGATGCCCCCAAGTTATCCACAGCCTCCTTCCGACCAAGACCTTATCCACCTGGAC TCCATTTTCCCTGTAAAGTTCTCCAACTGATCCTACCTCCCTACTCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCTTGTAACTACTGCTCTGTAC CAACTCCATCTGATGCCCCCAAGTTATCCACAGCCTCCTTCCGACCAAGACCTTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACTGATCCTACCTCCCTACTCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTTGTAACTACTGCTCTGTAC CTCCCTGCTCCTCTTCCCTGTGATGCTGCTCCTCAACAGCCGAAACCTGCTTGCATGGGGG GAGGGGGGCTTCTGAGTCTTCTCTTCTGCTTCTGCTTCTTCTTCCACAAACCACTTCTCAATAA GCCAAAATCTTCTCTTCTTCTCCCTCAGGCCACCTCCTGCTCCTCCTGCTGCTGCTGCTTTT CTGGA
D31762	82 G A		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAATAGCAGTGAAGTGAATGCAATTTGAGCTGTC CCAGGCTCTGTCTCCTCAGCTCATTTCTACTCTTTTCTTCTATATAACTCATTTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAGGCTGGGCTTTTCTGTAATAAGCTTCC TTT
D37931	64 T C		---	

[illegible]

EST33508					AAACATGCTATTGAACAACTTTTATAAGAG/GTAAAGTTGACTGAAAGCAGTTTAAAT
1a	36 A G			AACATCAACTCACAAATGACTTTTAGAGCCAAATAA
EST33863					ACAACATAGGACTGGTTATTTCTGGTTTGAAAAATATGTTGCCACTTCTATTGTTTAAAAATGA
4	77 C T			TCATTTAAQC/TTCTTTGAACACTACAGCCTGAATCCCC
EST34739					GAAATATCCTCCAGTGGCAGGAACCTGAGACTCCAGATCAACACAGGTGGACCTTTTGGTTGATGA
3	97 T A			GCTGATAGCTTCTAGGCTGTGGGGAACCTG/AGGTGCTTTACAACCTCAACTACTGCAGAAATTTCT
					TGTTTGCCTCATAAACA
EST34792					ACCTGACTGCTTTAAAGCTCTTTGAAGCTGACCGTAGCAGACATCACGTGGCATCCACTATCAATA
6b	104 A G			CTCATAGTCTAATTTATCCTCAGGATGTTCCCTGA/GGTATTCAGGAATTCCTTAGTCTCTATTACA
EST34835					AAGATTTTGTGCTGTG
9b	93 T G			GGAAATGTTCCTTTTGCCTTTGCAACAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG
EST34835					TGGGGAGTCTATGTTGCTTTCTGGT/GGGCCCTTAAAGAAACAGACAAATTTGTCTAAAGAT
9a	82 G A			GGAAATGTTCCTTTGCAACAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG
EST35230					TGGGGAGTCTATGTTG/ATGCTTTCTGGTGGCCCTTAAAGAAACAGACAAATTTGTCTAAAGAT
0	93 G T			CACAAAGTCCACTTTACTTACATGAAGAACATAAAGGCATGAGAAACAGTCACTCAATAAATG
					CAAGACATGAGCATAAAGAGGTTCTG/GTGGCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337					TCCTTTCAAATTTTGTAGTGGCATTAAATG/C/TTATAAATTTCTGCTTAGGAATGTATCTGCT
9	33 C T			ATATCTCAGAAAGTTTGGGCATGTTGTTTCCATTTTACTTAGTTTCAGAACTTTTCAATTTTTCATCT
EST35708					CTGCCCCAAATTAACTTTGGCAATGGAAC/C/TAGACTTACTGTATGGGACATTTTAAAG
9	32 C T			ACAGCTTAGTAATAATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGSCACCTTCTCTGTTGTG
					ATGTGCAAGTGTGGCT
EST35747					ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA/C/GATGTTTAAACGT
9	51 C G			TTCCCAACATCAACCTAATACAGTAGACAGCAACACCTCCCTCTGCCCCCTCCAGTAGGGTTGAGATT
					G
EST35751					TGGTCCATTATATTAACCTAGGGAAACACCGTGTGACATGGCAGACATTTATTTCAATGGAGA
9	89 C A			AGTTCTCCCATGAAACCAAGA/C/ACTTGTCTCATGATAAAGTGGAGACATAAGAAAGCCAGGT
					ATATAATTAAGCCCTGTGA
EST36301					CACCTGTTCTACTGGCTGCTATCTGTGGGCTGATGCTTACCAGTGTCTCAGCTACAGC
4	93 C T			AGTCAGGAGGCAGCCATGCCCTG/C/TGCTGATGGAGCTTGTAAATTTAGCCCCAAACGATCTTCA
					GAAAGAGGTACAAACA
EST36519					GCCATCAGCCCCACAAGACATGACTACCAAGC/G/TTGGCCCCCTTGACCCCATACTGGCCTCAGCAC
0a	33 G T			CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCCTCTCTCTGT
					CACAGGGGTCTTAGTGT

EST36620	50 GA	---	GAC TTATTAGATAAGGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGGGAGCTAGGGTTTAAAGG
6			AAGGCCTATTATTAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAAGACTTT
EST36690	89 CG	---	CCTGTGATGTGCATGGCTGAGCAGTGGTACTTACTATGGGTACAGACAGCTCACGTATGTCAGGA
0a			AAGGAAGTCTGGGGATTCTCAICGAGGGGACATATCACACATATCTTAAGTCACTGTGTGACTCGG
EST36729	62 CT	---	CTTGAGCAAGTCATTCTCA
9			GAGACAGAAGCATTACAGTTAAATGAGGTAGGCTTCCTCCTAAATATACATATGATGACAAATGCTTA
EST36823	103 AT	---	TATTAAGCCAGTAATGCACTTTAGCTACCCCTGGACATGCTATCAAGTGTGCTGGGAAGGGAG
6			ACTGTCTGCCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG
EST36987	126 CG	---	GTCAGTATCTCTGGGGTGTCTATTCAAGCAACAATTATTCCTTTATGTTCTTAAGCTCATCATGAG
4			TTAA
EST37054	88 TC	---	ATGATCGCTTATTAATTTGAGGGCGACATGGGTAAATGGGAGATACCCACAGACCTGTAAATATT
3			TAAATAATATTTAACAGCTGATCAGAGGCTAAATTTACAACTGACATTTTGATGCACTTTTCG/GTTA
EST37269	105 TG	---	GGGAATTAGACAATGCAG
33b			GGTCTCACTCTTGCCCGAGGACGGTTTGAACCTCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC
EST37284	93 GT	---	GAAAGTGTAGGATTACAGGTTCGTGAGCCACACACCTCGGTCTTGTTTAAAGTAACCACTGAA
2			C
EST37315	90 AG	---	AATAGTCTATGGCTACGGGCCGTGGGATGTTAAAAATTTGGATTTTAAATTAAGATTGTGAACATG
2a			CAAACCCAGCAATTTCTCAGCTATATTTTGAAGTCTTCGTGAGGAGAAAAATTTGGGTCC
EST37374	45 CT	---	AAAGACCTTTCTCAGCAGTAACCTTTGAGCAGAGACTCAGATGAAGTAAAGGATGAACCCAGGA
1			GGCTCTGGATAATGTCACTCTAGGAAGTGAATAACAGGTGTTAAACCCCTTGAGATAGCAACCCCT
EST37376	101 GC	---	CTTGGCTGCTTGAGGAATA
8b			AGATGGGTCTGCTAGCTTCTCGGGCTGAACTAAGATATCCTCCTCGCTCAGCCCTCCAGGTAGT
EST37376	90 AG	---	TGGAACTATAGTAGGAGTATCTTG/CCTCGCTGCTAGAACTTCAAGTTTTCATGGGCAATTCOA
2a			CCCCAGAGGACAGGACAA
EST37376	45 CT	---	CCTGCCATGATAATGTTAAACATATCAAGATCTCCTCAAACTTC/TAAGGGTGAAGAGCATACCC
1			ATTCATTTTATTGTTGAAATATTCCTTCACATAGCCAAACATTTTTTCAAGGCACCTGACTACTACA
EST37376	101 GC	---	GGA
8b			GTCACATCATGTCTCTCAATGCCCTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT
EST37376	101 GC	---	CTCTGGTTCAATCAGAGTGTGTCTGCA/GC/GCTGCTCCTCAGGCAAGTTGCTGACTTCTCTG
8b			TGTCAGG
EST37376	101 GC	---	GTCACATCATGTCTCTCAATGCCCTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAG
EST37376	101 GC	---	ACTCTCTGGTTCAATCAGAGTGTGTCTGAGGCTGTCCTCAGGCAAGTTGCTGACTTCTCTGT
EST37376	101 GC	---	GTCCAGG

EST37378	63	T G	ACACAAAAAATGTTGGCAGAAAATCTGGAAGATTCTTAATAACCTCAATTCTGCGTGAACATCTG
9	---	---	JAACATGCTCAAAAAGAGGGGAAAAAATCTTAACAGAAAACACTGTGTGACATGATTAGCTT
EST37452	46	G A	AAGACATAATCTGCAATGAATCAGTTATGAATAITTAACCTCTG/AJCTTCTCAGGAGTGACAC
4	---	---	TAATCATGCTGTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATAATCAATGACGTAGAA
EST37613	34	A G	CTAGGATGGGCTTTACAGTCATTTATAC/AJGTCATGAATTCATTATAAAACACACAGCGAT
6	---	---	ATAGCAATGAGCAAAACAGACCTCCCCAAAATCACCTCGCTGCTCATGGATCTTCCATCTAA
EST38025	56	T G	TTATTGAGTACCTACACTGTGGCCAGAACTAAGCTTTATAGGTGAAGACTCTGAGGTTTCAGAA
4	---	---	ACCATTTGAAAGGGTATTATTTCCCGCTCTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068	57	C T	TCTACCGACTCCAAAGATCTGTATATGCTTTAAGTGGCATTTTCATGTACATTATCTGCAATGG
6	---	---	AAGACGCTCTCCTTTTAAITCCCTAACTCTCTCTCTGGGAAGACAGAAACGTGGACAAA
EST38420	100	T C	TAAATCAAGGCCTCTTTCATTACCAAAACAAAAAAGGGAACAAATACGATGGGAGAGG
6a	---	---	GAAAGATGATGCGGAAGTGCATCCTGACTGACTGCTGCTCCCTGCAGTGCCTGCGGTCCTGCTGCT
EST38950	25	T C	TATTCATTCCTCTCTCA
5	---	---	TTTATTTGSCAAAAGTAAGCAGCCGGTCTGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG
EST39053	90	T C	CTGGAATACTCTGGGACTTTACATTTGACACAGGCTAAAGATATGGATGAGAGGAAACAAGACTT
6	---	---	ACAAACAAGAGCAGCCCA
EST39331	70	G C	TTTTTGTTACTCTGTAGCCAGTCATTAAATCTGAAGGTTTAAATATATCATTTTATTTGGGATGAGATCA
1	---	---	TAGTCTTTACACAAATGCTATGTCTG/AJAAACAAATGTTACTGAATATTTTACCCTCGTGGAGTTG
EST40544	31	C A	TCTCTCTCTCTAGCACTCAGACCACCAAGAACCCCTGGAAGACCGCCATGGAAGGAAAGTA
7	---	---	TGCTGCTGTTTAGGGAGAGCTGGCACCCTGCCTCTAATCTTCCCTCTGCCCATTTGACCCAGATGGT
EST40548	37	T C	GCCTTGGATACATCACT
4	---	---	GTCAACCATGACCTTACATATGTCCTGCTGTC/AJACCTATGAGGCACCTAGAACCTATTTGACTTCT
EST40549	42	A G	CACCTTTACCATTAGCTATCGAAGTTTGAAATTT
1	---	---	TTCTAATAGCATGCCCTGTGACAGGGAACCTAAGCTCTCTGCAAAATAACTGAACTAAATCTGTGA
EST40579	81	A C	AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTTGTAGTTTTTCTCCAGAAGGCTCAAGGTTTC
1	---	---	AATAATCTGTGGGACTCA
EST40584	58	A G	TGTTTCTAGAGAACCCTGTGTGATACACTACGCATGCAC/AJGATAAAGTCACATCAAGACTAA
2	---	---	TAATCTAAATGTTAGTTTGTACCACCATTTCTCACTTTTGAACCTAGCTCCCTGCAAGACACCTCTTA
3	---	---	CCCTGCACTTTTGGGGAG
4	---	---	TGTGAATTTACACATCAGTAAGGCAGTTTACAGAATTTTTCCTTACCTAAAGTCTGTGCTATCTG
5	---	---	AGTGGTGGAACAA/AJGSACTTTGGACACAGGATTTAAATAC/GGAACAAAGGCTTCTCCAGGAAG
6	---	---	TTGTAGTGTTAGGAATTTGGGAAGAAATTTATCTGTGGAAGGAAATTTGCCACCTGTAATGCACACCC
7	---	---	A/AJGTCGTACTGCCCAATATCCTATGTTTTAAGCT

EST51340	51 GA	---	---	---	GATGAAGTGTATTGCCAGGCCAGTCTCTGAAGAACTGTGAACATGAAGCAATGAAGTCTCAGGCTAGA AGGATAATGTGACCTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCCTCTCTAAGCTA GATAGCCCAAGGATTATT
J04182	134 TC	---	---	---	CATGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTCGAACCCCATCAT CCTCAGGCCCTCTACAAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCCTTTATCCAACTCTCGA TCCTTTCTCTGGTCTCCAGTGGAAAGGGAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT ASCTG
K01506	63 TC	---	---	---	CTGAAGTCCAGCTGCCCTACAAAGTCCATCTCAAGCTTTTCTCTCACTTCATGTGAAGCACTAQT/CJC CAGTGGCTGACTGAATTTGCTGACCCCTCAAGCTCTGCTCTTATCCATTACCTCAAGCAGTCAATCCT TAGTAAAGTTTCAACAATAAGAAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTTC ATTGAGCCCTTTTATCCT
L18877	69 TC	---	---	---	TGAGTCTGAGCAGCAGTTGAGCCAGGCCAGTGGGAGGAGTCTGGGCGAGTGCACCTTCCAAAGGCC CT/CJATCCATTAGTTTCCAGTGCCTGTGTGACATGAGGCCCATTTCTTCACTCTTTGAAGAGAGCAG TCAGATTGTTAGTAGTGAGTTCTGTCTTCTATTGGATGACTTTGAGATTATCTTTTGTCTCTGTGGGA ATTGTTCAAATGTT
L31848	36 TC	---	---	---	GCTATTTACATATCCCAAGCCCTTTAGGCTACAGT/CJCTCTTGCTCTGGACCCCTGTAGGGTGC TTTGAGTTTACAGCCCTAGAAAGAAAGGCTTTGGCCCTGTGTGGTGGCATAGGCTGTGAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT GT
L38517	137 GC	---	---	---	GGGTCCAGAAGCCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGAGCCTGAGCTGGGGGACACTGGC TCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGGCAACACCCAGCGTCCGCCAC CC/GC/CJCTGTGTGTAGTCATAGAGCTGCAAGCTGGCGAGGGGATGGTTGTGGACCCCTCT CTCTAGAGACCTTGAG
L39059	123 TG	---	---	---	ACTTTGAAGAGCAGAGCTGCCACCTCTCTGGAGCCACTGTGATGATGAGCCCAAGCAATTTGAGGCCA AGTTGAAGGGGACAGGCGCAACAAATACAGTAGTATTCTTTGTATTGTATATTTGTCGCTGA AGATCATCCCGCAAGGCGAGGCTGGAGGTGGCGCTGTGTCTGGGATTTTAGTCTGTGCTGG GAG
L412684	173 GA	---	---	---	CAAAGTTGCTCTCTGCCCATGAGCACACAGTCAAGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACATGGTTGCCAGTCCCAATGTACAGAGCTGGAACTTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCTCACACCAACAAATCTGAAC/GA/TGCTCTCCCTCTCCCTTGCATTACAATGTCT AAGGT

U05641d	166	C T	CTCCTCCTTTATTACGATGGAGGGTTAAATGGAGGATCCTTTTCTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAGAGATCTTTTACAACTTACCTTGTAAAGACAAAAT TATTTCCAGGCTATTAATACGTACTTTAGTC/TTTGAATTTATCTATGTCAATGATTTTAAAGCTA TGAATAATACAAATGGGGGA
U09607	39	T C	GAGGCCTTATGAGGGTCTCTACTTCAGGAACACCCCAATTCGACATTCGATTTGGGGGGCTCCCG TGCCCTGTAGAAATAGCCTGTGGCTTTGCAATTTGTAAGTTCAAGACAGATGGGCATATGTTCAG TGGGGCTCTCTGAGTCTTGCCCAAGAAAGCAAGGAACCAAAATTAAGACTCTCGCATCTCCCAAC CCCTTA
U09608	82	T C	GAGCAGAAAGGCAAGCGGCAAGATGAGTTTGGGGTTGTATTCGAAAGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCTTCTACATCTGCCCGCCCTTCAGCCCTTCCCGAGCCCTCTCTTGTCTTC ATTCAATCAACAAAATTTGGC
U10694	20	C G	GTGACATGAGGCCCATTTCTTCTGCTCTGTGTTGAAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCAGCAGTGTATGTCATCTCTGGGTCTCTTGTCTATGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATTTCAAAATGTTCTTTTAAATGGTCAAGTTTAAATGAAGTCACTCAGTGAAGTTAA TGAATGACAGTA
U13877b	162	T C	AAAAGACTCTGGTTCAATCCAGGTTCCATTTTGTATCTTTGTGACCTTGCACAAGTTGTTAAC CTCTTTGTTGAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGGAGGATTAGTGAAGTTACATGT AAAGCAGAGAGGAACAGCCCAAGAGATTC/TTACCGTGGTCTTACTAAAGTACATATCCTTAAGTGG GGTTACCTTTCAGCA
U15555	187	T C	TTCTGTCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCAATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAGAAATTAATAAGCAATGCTGAACATCAGGAATGTAGATATCCGTACAGAGAT TCCAGTAAATTTATGAGTCCAGCAGCCCTTTTCTAAGCAGTCTGGTCCATGT/CTGGTCTCATAC CTCATATGCAGGATTCATTC
U17077	122	T C	TCCAATTTATGTTCCCAAGAGAGCTTCCAAAGTTTGGCCATCTGGATGACAAACGGAGATCCACT AAACGTCCACGGGATTAACAGACAGTCTCTGACAGCTGCGGATGACACACACAC/CTTGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58	T C	GCACATGCAGAAATAGACTAGCCTATGCTCTGATTCAGCTGGGTAGTTTGAAGTTC/CTAGAG CTCCATCTTTTATGTTTATTTGTTATGTCCCTTCCCGGCTTCCACCTTAAATTTAGAGCTTTAA AGATGCACCTGCCAAATAGGACACAGATGGTGTAGCTGAAGTTTGAATAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164 C A	TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAGCCCTTTTAGTATATGAAATTAAT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAGCAATGACTATCTCTCG AAGACACCAAGAGAAATTCGCAAAAAGAC/AJAAGTATGACTTTTATGAAACCCCTTCTTTAGG GTCAGAGGAATTTGGACTGA
U25975a	143 C G	TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAGCCCTTTTAGTATATGAAATTAAT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAGCAATGACTATCTCTCG AAGACAC/C/GJAAGAGAAATTCGCAAAAAGACAAATGACTTTTATGAAACCCCTTCTTTAGG GTCAGAGGAATTTGGACTGA
U25997	61 A G	CAGGAGAGGTTATTCAACCTCACAACTAGTATCATTTTAGGGGTGTGACACACCA/A/GJTT TTGAGTGTACTGTGCGGTTTGATTTTAAAGTAGTCTTATTTCTATCCCTTAAAGAAATTT GCATGAACCTAGGCTTCTGTAATCAATATCCCAACATCTGCAATGGCAGCATTCACCAACAAAA TCC
U28413	29 C T	ATTCTGACAGCTAAATTAGCCCTAAATG/C/JGGGTAATATTTTCCCTCATGTTTAAATGAGGT AATATTGCATAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCTTGATCC CAGATGTTGGCCTGGGAAAGCCCTCATTTGTACAGTACAAAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89 A G	TAGGGTAGCATTAAAGATTCAGGATCATTAGCAGTGTGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATTCCACGTAGCC/A/GJTTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACITGCCACACAGTTGAACACAAAT GCTGTCA
U30884a	34 A G	TAGGGTAGCATTAAAGATTCAGGATCATTAGCAGTGTGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTCCACGTAGCCAAATGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACITGCCACACAGTTGAACACAAAT GCTGTCA
U31216b	78 A G	GGGACAGCATATGTGGACCCGCTCTCTGTGCAAGTGAAGACCAATGAGACGGCTGCAACCAACA GCCGTATCA/A/GJCCCTCACTAAAGTTACCAAGGCTCTGCAAGAGCCCTGACCTTTTCAGATA CCAGCACCAGACCCCTTACACGTAGAGGAGGAGGATGCCAGCAGTGGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A	GGGACAGCATATGTGGACCCGCTCTCTGTGCAAGTGAAGACCAATGAGACGGCTGCAACCAACA GCC/GA/JTCAACCCCTCACTAAAGTTACCAAGGCTCTGCAAGAGCCCTGACCTTTTCAGATA CCAGCACCAGACCCCTTACACGTAGAGGAGGAGGATGCCAGCAGTGGCTTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ...			AGTTGCCAGCTCCCATGTACACAGAGCTGGAATCTGAAGCGGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCACTG/AJCCACAATCTGGTGCTCTCTCTTTGCTTACAAATGTCTAGTCCCACTGCCTGCT GGAAGAAACACACTCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ...			AGTTGCCAGCTCCCATGTACACAGAGCTGGAATCTGAAGCGGTGAGTCTTCATCTTAGGGCATCGCTC C/ TCTCCTCAGCGCAAAATCTGGTGCTCTCTCTTGTACAAATGTCTAGTCCCACTGCCTGCTG GAAAGAAACACACTCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ...			ACGGGTACACAGAGAAACCTGAGTCTAGCCATTGAGGGCTTATGCTCCCAACTCACATTGCTCCTCC AGACCGCAGG C/ TCCCCAGGCTCAGGTTGCTGGAGCTGTACATGACTGCACTGCTGCTGCCAGG GCTCAAGCAAGTCTTCTCTATCTGGGGACGCTGCTCGAGAGGCGCGAGAGCGCCGAGAAC ATGCCAGGTGTCC
U37690	54 A G ...			GACCACTGTAACCCACCCACCGCTGTCTGCTACCATGGGCTGAGCGTCTTGAJCCCGGAAATC ACGAGGCTGAGGATCCGGGAGCTGGCGTAATGCCCTGGCCGAGTGTGTGTATCCCATACCCACT CTGGAAGGAACCATCCAGTAAAGGTCTTT
V00540	39 T C ...			TGAAACCGTTTCAACATGGAAATGATCTGTATTGACTAATTCACACCATCCACACTTCTATGACT TCTGCCATTTCAAGACTCATTTCTCCTATAACCCAGCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ...			TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCTCTCTGAGACCATGTGGTTTTTAAATATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTTCCAGTAGCTAAGACCCTAGAAATTTGGATTCTCTGTTTTTTCATGCTCTCCTTT GTAAACCTGAGATCATCAG
X52011b	148 C T ...			AGGAAGATCCACCGACCCCTCCTGGCTTATCTTTAGATTAGGTACATTAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACATTCACAAAGAAAGTTGCGAAATTTGCG AAATCTGTTGTGCA C/ TGTCAAATGAAACGCCCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 A C ...			AGGAAGATCCACCGACCCCTCCTGGCTTAACTCTTTAGATTAGGTACATTAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACATTCACAAAGAA A/C GTTTGGGAAAT GCGAAATCTGTTGTGCACGCTCAATGAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X87344	34 CT	...	CATCCAAAGGCACTGGTGGTACTGCTCTCTCTGCTACTGACCCAGAGCCTCTGCTGTGCACCTGC AAGCTGTGTCTACTGAGGCCCCAAGGGGACTCTCTGTTTCCATCTCCCCCCACAGACCTGTCAAGAG AAGCATGACAAACAAATCATTTACCGACTTTAAGTCTTTTTT
X87838	179 GT	...	GGTGGCTGTATCTCAGAAAGTGCCTGACACTAACCAAGCTGAGTTTCTCTATGGGAACAATTGA AGTAACTTTTGTCTGGTCTTTTGGTGGAGGAGTAACAATAATGGGATTTGGGAGTGACTC AAGAAAGTGAAGAATGCACAAGAATGGATCACAAGATGGAATTTA/GTCAAACCCCTAGCCCTTGCTT GTTAAATTT
Z14138	81 AG	...	GTCTGCTGCCCTCTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA CCTCTGTGACCCGAGTGAATGTGCTCCCAAGCGGCCCTGTGTGTTTGACATGTGAAGCTATTTGAT ATGCACAGGTCTCAAGGTTCTCATTTCTCAGGTGACGTGATTTCTAAGGCAGGATTTGAGAGTTTACA GAAGGAT
Z18859	191 AC	...	TAATCCTCACCATCTCCTCAGGTAAAGTTCTATAAACAGGCTTGGAATCTGGGTAATTAATAACAGA AAATTTATAGTCAATATACCATGACATGAAGAATGAATCCATCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTACATACGTTCTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGCAGCAGGTTTC CAGTACTGGTTTCCAA
Z23091	159 GA	...	AGAACTGACACAGATGTGGCTGGAGGGGAATCCAGACCCGCTGCTGTCTCTCTCCCTCCCTCCC CACCTCCTCCG CTCTGTGCTGAAA CTGAGCTTGACGTTTG
11595b	125 AG	...	GTGGCAATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCTAGTTGTCTCCAGGACCTAAGJGGGTGC TCACCTACCTTGTCTTTGTGTGAAGGAGTGGTTCCCATGACTGTTTAAAGTGACAAGTGCCCATGG ATATCTACACCGTCAACAGACTAGATTGTCTCAATGTCTCTGCTTGGCTTGGCAG
11595	125 AG	...	GTGGCAATTGTTAGTAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCTAGTTGTCTCCAGGACCTAAGJGGGTGC TCACCTACCTTGTCTTTGTGTGAAGGAGTGGTTCCCATGACTGTTTAAAGTGACAAGTGCCCATGG ATATCTACACCGTCAACAGACTAGATTGTCTCAATGTCTCTGCTTGGCTTGGCAG
1241 131 GT	TATATCACATTAGTATGCTACTGCCATGTAAGGACTTTGATCAGTAGGAATTAAGAACACTTTTGAA TGGTCTTGTCTCTTCAATAAAAGAGTGAATGATTAAGGAGTGTGTTTAGATTAAGGGCAGCTTGT JGAGGAGTGTGATGATGAAGAGAGAGATTAAGGAGATCAGGAAGAAAGTAGCAATGGGA ATGAAAATAGGAGGCTGAGATCCACTGGATAATCTAAATAACCAAGAGAAAG

1282	130 C T	GTGGATCACCACCTACAGTCTAATTTTCAGATGTTTTCATTACCCCTAAAGAAATCTGTACCCATTAGCAATTAATTCCTCAATTCCTGCCCTACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGCCQCTACTTGACATATACATACACATGGAGCCATACATATGTGTGCCCTTCATGATGGCTCTTCACTGAGAATAATGTTTCAAGGT
6810	68 C T	AGTATCACACATACCTTAATATATATAGATATACACAATAATAAATCACTCCCTACCTTGAAACITTTAC/TJAGAAGCATTTTAAATTTTACAAACAAGCTCAACGAACCTACAATAAGCTAGTAGTCTGTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTTAAAAATGTCTATGAACAAGTACAAATTTCTTTTGTAGTCTGCAGAGCAATGACCACCTAAGAAATATTTTAAAGGC
6817	118 A C	CCAAGTACATTTGGTGAACGATGAGCTAGCTGTCTAGTATTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAAATCATCACTCAACAATGTAGCTGAGGTAACJACJGTGGATACCCCTGTGTGCTCTACTGGCTCCAAAGGCATTCAGGGGATCATCAAGATGTTGGACACCTTGTGTCAAAATCTTGGTTCAGGTGGGCTGTGCAGATCGGCTTTTGGTTGGTGTCTAG
6819b	212 C	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGCGAGGAGCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCTCTCAACAGTTTTCATATACAAAATTTCTGCTATTTTGTCTTAGCAAAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166 G T	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGCGAGGAGCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCTCTCAACAGTTTGT/CATATACAAAATTTTCTGCTATTTTGTCTTAGCAAAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
681xx	39 A G	CTGGTATGTCATAAGCAATCCATAATTTGTATAGCTATTTGTTATCTATGGCACCAATTTGGGACACAGATTATATGTGACAGACCCAGCAATGTCCCTTAAGATATGCGAGCAACACAAATCTGTCATGGTTAACAAAAGAAATGAACGTCTAGG
6972b	149 G T	AGGATCCCTCTTTTCTATGATTGGAATGTTTCAGAAGGAATGGTACCAAGTTCCCTCTGTACCTCTGTAGAAATTCGGCTGTGAATCCATCTGGCTCGACTCTTTTGGTTGGTAACTATGATTATGCCACAATTCAGAG/GTCCGTGTTATGGTCTATTCAGAGATTCAACTCTTCCTGGTTAGTCTTGGGAGAGTGTATGTGCGAGGAAT
6972a	122 A G	AGGATCCCTCTTTTCTATGATTGGAATGTTTCAGAAGGAATGGTACCAAGTTCCCTCTGTACCTCTGTAGAAATTCGGCTGTGAATCCATCTGGCTCGACTCTTTTGGTTGGTAACTATGATTATTTGCCACAATTCAGAGCCTGTATGGTCTATTCAGAGATTCAACTCTTCCTGGTTAGTCTTGGGAGAGTGTATGTGCGAGGAAT

7598k	210 A C	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCCT CAATGCAG[A/C]
7598j	208 A T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCCT CAATGCA[AT/GA]
7598i	192 G T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598h	144 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598g	142 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598l	120 A G	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598e	83 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCCT CCTCAATGCAGA
7598d	77 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGAATTTACCTTGGAGAAATGAAATTTATTTCTTGAGGATGCCCTTTTA TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATTTTCCCGTATTTTCCCT CCTCAATGCAGA

7598c	56	A G	AAAGGTAATCAAAGTCCCTCTATAATATTGAATTTACAAAAGACACCCAGCCAA/GJAGGAAC TCAATGAAATAGCCGCTAACGATTTACCTTGGAGAAATGAAATATTCTTGGAGATGCCTT TTAATATTGATCCATTATGTGAGAGATTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47	C G	AAAGGTAATCAAAGTCCCTCTATAATATTGAATTTACAAAAGACACCCAGCCAAAGGAAC TCAATGAAATAGCCGCTAACGATTTACCTTGGAGAAATGAAATATTCTTGGAGATGCCTT TTAATATTGATCCATTATGTGAGAGATTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30	A G	AAAGGTAATCAAAGTCCCTCTATAATTTAGTGAATTTACAAAAGACACCCAGCCAAAGGAAC TCAATGAAATAGCCGCTAACGATTTACCTTGGAGAAATGAAATATTCTTGGAGATGCCTT TTAATATTGATCCATTATGTGAGAGATTTCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116	A T	GTGTGATCTCACTGGGTGCTGCAGGCGCGAGGTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGATGCTATCTTCTCAAGGTCCCAAATTAATJCCCTTGGAGTTCCCT GTGTGATCTCACTGGGTGCTGCAGGCGCGAGGTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGATGCTTACJCTCTTCAAGGTCCCAAATTAACCTTGGAGTTCCCT GTGTGATCTCACTGGGTGCTGCAGGCGCGAGGTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTATGAATGGGTGATGCTCTTCTCAAGGTCCCAAATTAACCTTGGAGTTCCCT AAATACAGAAATTTTATTAGAAATCTGTTTAAAGTAGAAAAAACCCCTGTCAAAGAACCCAGGTGG AAAAATGGGTCCCAATAAATGGAATTTTAGGGCAACAAAGTCAAAGGCCAA/GJCAAAAGAGA AATAGCACCACTGTCTTTGAACAAATGCTAGTACTTGCATTTTGGCATTTGTAAATCACTGAATC TGGGTTTCTCTGTAATTCACACAGAGCATGCACACACATTTTATCAT
8467b	93	C T	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTAA/CJTGCTATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAGATTAAGGAAAAAATTACTG AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCATT TGAGCGCAAAATCCACTTTGCTGTAAAGGTCATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAGATTAAGGAAAAAATTACTG AGGGTTACGGGTTTGGTTTAAATCAGGCTGCACACCTTTCAAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG/CJTAATACTTCAATAATCGAAAAAGAAAAAATTCCTTAAGGAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGTCTTTAAATAAAGAGGGGCTAATGTTTCATGTTGCT TTATACATCTCTCTCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG
8467a	70	A G	
8498	84	C T	

WI-18562	29 GA ...	---	---	CTAAGGAAAAATTAATGATGGAATATC(G/A)ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATT TAGCATTAATCAGAAACGA
WI-18618	51 AC ...	---	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGCCGAGCTAAGAAC(A/C)CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCCAAAGTATAAATGTAAACCCACAGTGCCTCGACAGTTC AC
WI-18683	22 CT ...	---	---	TAAGCTGTTGAGGACTGGACTGCTGGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCAAAGCCTGCCCTGAGT
WI-18520	75 GA ...	---	---	GACTTGGTGATTTAATGCTTTCCCTTAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACAG(A/C)CCGGAGTGGTAAATACTACTACTGCAACAAACACGGGCATCCACTGCTCTCA TGCTCTTCCTGGAGAC
WI-18563	94 AG ...	---	---	AAATAAAGTTTTATTGGCACAGCCAGCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAG(A/G)GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18562b	69 TA ...	---	---	GTCTATTCAATTTAGCTAGAACCAATTTCTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC T(A/G)TGCCATAATTTAATCAGTGCCTAATTTGAAAGACATTTGGATCGTTTCCAG
WI-18723i	94 GA ...	---	---	AACTTTATTGATCTGACGATCAGGATAGTTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGTTAACAGGTACATAGGTAAACCAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71 TC ...	---	---	AACTTTATTGATCTGACGATCAGGATAGTTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGT(C/A)ACAGGTACATAGGTAAACCAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96 AG ...	---	---	AACTTTATTGATCTGACGATCAGGATAGTTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGTAAACAGGTACATAGGTAAACCAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44 GA ...	---	---	TTTATTACAATATTAGTGGCACATAAATAAAGCTTCTGA(G/A)ACAGGAGGTAAACATCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAATA
WI-18715	76 GA ...	---	---	TTATCAGAAAAAGTGATATTGACAGGGTCTGGGGCTGTACATGGCAGGGGCTGGTGAGCTTTG TACATGGG(G/A)CTGGGAGACAGGAGGCCTCCAGGTGGAAGGTATTTTTTAATAAAAAATAA TGGAGCTACACACACCC
WI-18535	107 GA ...	---	---	GTAATAAAGTTTTATTGGCACAGCCAGCTGTTTCATTATGCCATTGACATCTGCTGTGCOCT ACACAGCAGGGTGGGACCTGCTCTTCCGGGAGAGCTA(G/A)TTGTTTAAAGCAGTGGTCCCCAAC CTCTGTGGTCCCGGTG
D17525	107 CT ...	---	---	AGAGTGGTCAAGACACAGCCGAAATCCAGGCTTATCACTTACTAGTTTTCAGTTCTGGGCAAGTGAC TTTATCTCTTCGAACCTTCAGTTTCTTCAAGATGGAA(A/C)TGCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAAACAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAGGTGATGTCTACCAAGCCAGCAGGAAG

DWU-133c	313 A G ---	---	---	TAA TTGGCCACTGCCTTATTATTACAAACAGAAATGTCTCATGACTTTTATGTGTGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAAGTTTGAATTTTAAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C ---	---	---	TAA TTGGCCACTGCCTTATTATTACAAACAGAAATGTCTCATGACTTTTATGTGTGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAAGTTTGAATTTTAAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T ---	---	---	TAA TTGGCCACTGCCTTATTATTACAAACAGAAATGTCTCATGACTTTTATGTGTGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGGAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTCAAGTTTGAATTTTAAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T ---	---	---	ATGAGATCCTTTAAATCCTTCATGAAAGCTTTTGTGGTGGCCACTCCTACGCTCAACATGAAGTG TGTTTCTTCAGTGCATCTGGGAAGATTTCTACCTCTGACCAACAGTCTCTTCCAGCTTCCATTTGCGC CCTCATTTATCCCTCAACCCAGCCAGCCAGGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAGGATTCATGTGGAAATATAAAGAT
DWU-387	169 G T ---	---	---	GTGTATAAATGCAACTGTGTTTCTCAACATGGCTCACAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTGTGTTTAAACTGCACTGCCAACAAGTTGATGATAGCACAAGCTTAGCTAATCAA CTCTTTTGAGGTGAATATAATTTATATTACAATG(GT)AAAAGCTCTTTAAATAGTAATTTTCA GGTCTCACCAGTATCAAGTAAATACACAAATGAAGTGTCAATTAITCAA
DWU-447b	172 --- --- ---	---	---	ATTTAGTGTCTTGGCTTAAATAATCATTTGAAAAGTATTTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATAGTTGATGAGCACAAGCTTAGCTAATCAA CCATTTTTCATTTTGTGTTCTTAAGAGGATGANAATCAGTTTAAATGTCTTCTTCTGTTAG GCCTTTCTTCTTACAATGAAGAGATGATTTCTTAGTTTATGGTTA
DWU-447	85 A G ---	---	---	ATTTAGTGTCTTGGCTTAAATAATCATTTGAAAAGTATTTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATAGTTGATGAGCACAAGCTTAGCTAATCAA CAACCATTTTTCATTTTGTGTTCTTAAGAGGATGANAATCAGTTTAAATGTCTTCTTCTGTTAG TTAGGCTTCTTCTTACAATGAAGAGATGATTTCTTAGTTTATGGTTA
DWU-476	63 C G ---	---	---	GTAAATTCAGTTTTCAGTCTCTTTTGTGCTCTTCTCAATAGCGTTTAAAGGTGAG(C)GAT AAATCAACTGCCATCAGGTGAGGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTCTGGGAGATTTT

DWU-505	67 A T	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCTACACAGAAAATCTATCACCATACAAAATTTA A/TTCAGTATTATGTTTAAAGCACACAGGTGTACCGAAACTGTGAAAGTCTGAAATTTATGGGTT CTATGCATGCAATTTTGCTTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGGACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G	AAAATCCAGGCAATTCGAATCTGTTTTTCATGATTATAGAGGGTTTACACAAAGTGCCACTTATTA AGAGCTTCCACAGTGAAGATGGAGAGGTGAACCTTGCTTTGAATATCCAGATGTGTTGGTGAAG TGCGTATGGCAGTGAGCAGGTATGTTGCTTTGCTTGCTGCACTGAAATTTAAATTTGCTATCAAGAGC AAATATGAACGGTTTTTTTATCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C	AACTGCATATAGATAATATCCAGGATGTGGCTCATTCTTTTCAGCTTGTTTCTATCTACTGTTGTA ATATACAGTTTTGTGAACCATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTAAAAATAACATATCTTGCTTCAAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTCG
DWU-59	94 C T	CATTTCTTTGTGAAGGTAAATGGACTCAAGGGGGAAGAAACATGCTGAGATGGAAGTCTACCCG CCCTTTCTTTGTGAACGTCAATTTGGC/CJTGAGCCGTGTCAGTTCCAGGTGCAGACTCGTTTTCG GTAGTTTGTTTTAACTTCCAGGTGGTTTAACTCTGATAGCCGGTGAATTTCCCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C	CTTGATCATGGGTGGAAATTTTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T	CACACTGCGATCTAGGCTTTGGCTTGCAATTCAGAGGAGAGAGCCAGTCCCTCTCTGGAGA/CJTG CTGCGTTCCCGAGCCCGCCACACCGGCTTTGCAACACAGAGCTGTTGAGCAGAGGTGGTGAAGAGCT AGCTGTAGACCCCAAGCAACACCCAGCCCTGGGACCTTGCGGAGAGGAGCAGCTTTAGAACATGGAA AAGTGTGGTCTATCCCATCATTAGACAAGACACATCTACATAATAAAAGT
WI-18014	40 A G	TCCATTTACATTTGGTGGCAATTTGTTGAATAGCTACAGAA/CJGAAATGAAAGTGCACCATCAGAGT GTAATAGGCTGTGTGAACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCAGAGTGGAAATTTTAACTTCTTCAAT/AJCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGATCTGAAGG
WI-18036a	27 T C	TTCCAATGTAAGAGTCAAGTACCAAGTT/CJAAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCAGAGTGGAAATTTTAACTTCTTCAATATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGATCTGAAGG
WI-18046	72 C T	TGTAAGGTGACTTCTATAAGCTTCTAACTGCAACTTTCATTTACTGAGATTATTTTCAGGCCAAT GTG/CJTTGTTGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACTGTTCTCTGTTTCA

EST5	93 A ---	---	CTGTGGGAGAAACAAATTTGGTATATTCATACAATGTGAACATCTTCAGAAATAAGAAAGAA CAAACTGTAATCACACACATGGACAAATCTCAATCATTTATGCTGATGGAAGAAACCATTTCA TAAGAAATACACAGTACAT
EST6	48 C ---	---	TTAGCTACTTTTCAGAAATTTGAAGAGAAATGCAATTTGTGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTCTTTTGCACAGACAAAGCCACATTTTGCATTAGACAGAT
EST8	158 A ---	---	GGACAGGACCTCTATTCGCGCTGGTGCGAGCAGCGCTGATGACTGAGGCCCCAGGGACTACTGGGCG CTCTCTCAGGGGCTCTCCAGAACCCAGAGCTTCTCTCTGAGTTTCCCTAGAGCTGTGGGCGCA GATAGCTGTCTCTGAGTTGCAAGCACGATGGAGATTGGACACTGTGCTTTTGGTGGGT
WI- 18740c	104 GT ---	---	TCCTCATTGTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATCCAGTAGTG/TAATAATCATTTTGATGGCTTCTATTT TGGCCA
WI- 18740b	96 C G ---	---	TCCTCATTGTGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATC/G/AGTAGTGATAATTCATTTTGATGGCTTCTATTT TGGCCA
WI- 18985a	105 CT ---	---	CCAAAGTCTCTGTTCGCTATAAGAGTTTGGGATGGGAGAGATCCAGACCATCTTGGGCGCA GCCAGGCCCTTGCCTTCATTTACAGAGGTAGCACAA/C/TTGATTCCAACACAAAACCCCTTCCOC TTTTAAATGATTCTGTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTGTTTCTCTT TGAAGCAATGACAAAGCACTTACTTTCACGGTGTGTTTTTCTTAT
WI-18746	114 GA ---	---	GCCAGCAGCTGAAGTCTCTTTCTCTCTCTGCGCTGGAAGACATCAAGATACCTTTGCGTGGATCA AGCTTGTGACTTGACCGTTTTATATTACTTTTGTAAATATTTT/G/ATCCACATTTCTACTTCAGCT TTGGATGGTTACCG
WI-19112	212 GA ---	---	CCGTTCACACACACACATGGCAAGCATAGTCGCTGGTTACGGCCCCAGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGTCTATCTCATGACAAACCCACAAAGAACCCGACGACAA TCTTTTGGGAGATTTCTCTCTAGTGGCTTGAAGACATGGCTTTAAGAACACCGGTATATCTTTGAG GGTGACAAGGG/G/ATCTCTTCAACAGTTCATACCAACTGCTTCTCTAG
WI-19092	232 AC ---	---	TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCCTCTATAAGAGGCTATCTTAGATCATGT CTCAATGGAAACACTCTCTCTTCTAGCTTACTTGAATCTGCTTAAATAAGAGTAGGACACACAC ATTGAAGCTCTGATCAACGGCTCGAAATTTTCTCTTGAATGTCTTTTAACTGAATTTTC TTTTAAGCTAACAAAGATCATATTTT/CAC/ATGATTAGCCGTGTAAC
WI-19057i	175 GA ---	---	CCCATTTTATAGGCCAGTGTCTCAAGAGTAGAGGCGTCTACTGGTCTTTCACCTCTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGAAGTGGTATTTGACGTCAGGACCCGACGCGACTG TCTTCATGACAGGAACACAGTGGCAGATCCACAGCTG/G/ATCTCTTCTATCTTTGTTTGGCCACA

WI-20103	168	C T	---			TGGGACTTCCAACCTCAGAGGATGTGGGAATCCACGTCAAATGATACAGATAAATGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTATGGGTCAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGGAAGCTGGGTCTCCCAACCTTTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGTAGAGCTAGCCTAGCTCATCTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTTGCACATATATACATATGACACCCTTTCAGTGGCAACATATATCCACACTA TAAACATACCACATTTATAATCTGTAGGACAAAGAAATGGAJTTGAATAAGTACCCCCCAA CATATACAAAGAAAGTTAGCATACTTACCCCGTTTTCACATCATCAGAGGCAAAATAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A G	---			TGGTTACAAAACCTAAGCCATATACAAAATAGGAACACATTTAGATGCCCTCTTTTGAAGAACGT TTTAGTCTTTTAACTGAGTTTAAAAAATAACAAATGCAATTTTAAJGJACACTGTTTGA ACTTAAAGTGCACAAATA
WI-20813c	165	A G	---			GTCTCAAGGGGGAGAAACCTGGTTCTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGSCATGGGAGGAGGCGAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAJGJAAAGGAGTTTCCACGCCAGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCTCAAGGGGGAGAAACCTGGTTCTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGSCATGGGAGGAGGCGAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAJGJAAAGGAGTTTCCACGCCAGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAGAGTGATTCAGTTGCAGTAATACACTGCACAGGTAAATAJGJATACATTAGAAAA GCAAAATCTTTTAACTTAAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAAATACAGG TAGGCAAGAGTTTCCACACTGGAAATGAAGGAGTTTCCAAATCTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCAGTTGGAATATGGCTATACGAACCAAGAGTGTATACAAATGGAAGTGGTCATCAGGCAATA ATTGTTCTTCTTGAAGTCTGCACGAGTGTCCATGCTCTGTGGGAGCTTACACATCAAGTTTGACAG T/CJTGAACCAACTGGAGTGTCTTTCCAAAGAAATGTCTGTGCTCTCAATAGGAATTCATG TTATTTCTTCTTGGCTTAAAGTCTTATATCTTCAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCTGJAAAGCTGGGAGCGT GGGCTCAGCAGGCTGGTCACTCCATCCCGTAAGACCTCTCCCTCTCCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGGCTTATGATCCCAACACGCTCTTGACCAGGTGCTCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTACAGTGTCTTTAAGTAAAAATGGTGGAGAAAGGACACCGJAJGGAAGCGG TCTGGGCGCTGGCAGTCCGCGGAGCGGAGTGGTCTGGCTGTGTGAGATCTCAAGGAGCGAGCAT GTGCTGGACACACAGACTATTTTAGATTTTCTTTTGGCTTTTGGCAACC

WI-20146	31 T C TGAGTCTTGTGAATTCATTGAGCAGTTAGTTCATTTGAGATAAAGTCAATGCCAAACACTAG CTCTGTAATAATCCCATCATTAATGTTAAAGCCTCATTTGAAATGTTGAATTCATATACAGGC
WI-18922	74 G A TAGGAATTGGTTTACGCGCTGAGGCAATTAGACACTTTTGAAGATGGCATAACCTGCTCACCTGGAC TTAAGC/GA/TCTGGCTCTAATTCACAGTCTCTTTCTCTCCTACTGTATCCAGGTTCCCTCCAGAG GAGCCACCACTTCTC
WI-18763b	53 A G TTCTGTGTTGTGGGTCACCGTACAAATGGTGGGAATGACGATGATGTGA/AGTATTTAGAATG TACCATAATTTTGTAAATTAATTTATGTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA TGTGTTTGGCAA
WI-18763a	38 A G TTCTGTGTTGTGGGTCACCGTACAAATGGTGGGA/AGTACGATGATGTGAATTTAGAATG TACCATAATTTTGTAAATTAATTTATGTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA TGTGTTTGGCAA
WI-18771b	75 G A CTCATTTCCATGCCATTGTGGAATTGACGAGAACCTGCTCTCGAGGATGCTAGAAATGTTGGG AACAGAA/GA/AAATAAAGTGAATTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G CTCATTTCCATGCCATTGTGGAATTGACGAGAACCTGCTCTCGAGGATGCTAGAA/AGTATGTT GGGAACAGAGAAATAAAGTGAATTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C GGGAAAAATTTGAGACGCAATACCAATAGGATTTTGGTCTGGTGTGTTGATGAAATTTCTGAG GCC/TCTGATTTAAATCTTTCATTGTGATGTGATTTCCCTTTAGGTATATGCGCTAAGTGAACTT GTCA
WI-18742b	51 C T ACAAAGTCCTGTAGCCCCCTCACCTTTCTGTTTACCTTTTGCCAAATGATC/TATCGGGTTTGGTTT TCTGTGTAATTTAAACGGTTGTGGTTTCTTTTCCACGGAGTTCAAGTAAAGCCCTGCAGGAGA GTTTAC
WI-18882	94 C T GTGTGTCAAAAATGGGGTCTGCTCTGCTACCTTGACCCCTTCCCTTCTCTCTCTCTCTCAATCA TCAATCCCAACAACATCCTCTGCCA/C/TACACAAACAAACGTAAGTTTCAATTTGGGCAAAAAATTGA GC
WI-19970b	167 G A TATAAGCCCGAGTACACGAGCGGCTGTCTGGCCACAGACAGGGGCTGCTGTGGAGCCTGCCACCC GGCCCGCGAGTGCAGTCCAGCGGGAGGAGGCTGCCGTTCTCCAGTTCCTCACTGCGGGAGCC AGCAAGGCTTCTCACTGGTGGTCAAG/GA/ATAGTCACTTGGCTGGCTGCATCCACAGAGGA TGTGTTCAACACAGAAATCTTTTAAACGACTGACCTTCTTTAAACACAGA
WI-19970a	126 T C TATAAGCCCGAGTACACGAGCGGCTGTCTGGCCACAGACAGGGGCTGCTGTGGAGCCTGCCACCC GGCCCGCGAGTGCAGTCCAGCGGGAGGAGGCTGCCGTTCTCCAGTTCCTCACTGCGGGAGCC ACCAGCAAGGCTTCTCACTGGTGGTCAAGGTAGTCACTTGGCTGGCTGCATCCACAGAGGAT GTTGTTCAACACAGAAATCTTTTAAACGACTGACCTTCTTTAAACACAGA

WI-19067d	202 T G ---	---	TAITGCTGTTGTCAGTGCCTGACATTACGGCAGAGCAAGGCTGCTCAGCCTCCCTGGCTGTCACATTCCCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGATCTCAGTGGGTTCTCTGGGCTAGGCTCGGAGAAATGTTGAGGGGTTATTTTTTAATAGTGTTCATAAAAGAAAT/GJACATAGTATTTCTTCTCAAGACGTGGGGGAAATATCTCATATC
WI-19067c	153 G C ---	---	TATTGCTGCTGTGACGTGCTGACATTCACGGCAGAGCAAGGCTGCTGCAAGCCTCCCTGGCTGTCACATTCCCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGATCTCAGTGGGTTCTTGCCGCTAGGCTGCTG/CJAGAAATGTTGAGGGGTTATTTTTTAATAGTGTTCATAAAGAAATACATAGTATTTCTTCTCAAGACGTGGGGGAAATATCTCATATC
WI-19067b	151 T C ---	---	TATTGCTGCTGTGACGTGCTGACATTCACGGCAGAGCAAGGCTGCTGCAAGCCTCCCTGGCTGTCACATTCCCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGATCTCAGTGGGTTCTTGCCGCTAGGCTGCTG/CJAGAAATGTTGAGGGGTTATTTTTTAATAGTGTTCATAAAGAAATACATAGTATTTCTTCTCAAGACGTGGGGGAAATATCTCATATC
WI-19067a	57 C G ---	---	TAITGCTGCTGTGACGTGCTGACATTCACGGCAGAGCAAGGCTGCTGCAAGCCTCCCTGGCTGTCACATTCCCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGATCTCAGTGGGTTCTTGCCGCTAGGCTGCTG/CJAGAAATGTTGAGGGGTTATTTTTTAATAGTGTTCATAAAGAAATACATAGTATTTCTTCTCAAGACGTGGGGGAAATATCTCATATC
WI-19106	247 T C ---	---	TAATCCAGCCCTACCTGTTAGTATTTAGGACAGCTGACGACATGAGCATAAAGGCTGCTGCTGCTGCCAGAGACTGCTCCGCCATCCACAGATGATGATCTCAGTGGGTTCTTGCCGCTAGGCTGCTG/CJAGAAATGTTGAGGGGTTATTTTTTAATAGTGTTCATAAAGAAATACATAGTATTTCTTCTCAAGACGTGGGGGAAATATCTCATATC
WI-18944	147 A G ---	---	CAAGCAGAAATATCAGAGCTTTTACACACCTACTAAAGAAATTTATGATGCTGAAACAAAATGCGCAGAGGATATGATGCTTACATCTTTAACTAGTATTTACCTAGCATTTCAGGCTGTTGGTGTCTGTGTAATACAAATATTTAGCCCTTCTCAGCTGTAAGGAACTGGGTTGGTGTCTGTGCTTTTAGAATTTATGTTCCCTGTTGGGATGAGTTTAAATGCCACAGACATAATTTAATAAATAAACTTTGGGAAAGGTGTAAG/AJACAGTAGCCCTCATCAT
WI-18952	232 G A ---	---	CACACCTCATGCTAGCCTCAGCAAACTGGAAATAGCCTTCGAAAGAAATGCTTCTGAAGCTTGTACTGTATATCAGTGTAGAACTGTTGCTGATTTGACCTGTATTAAGTTAACTGTTCCCTGTGATATCAGCTGTACATATCTTTGAGTTCAG/CJCTTTAGTACGTTGGCTGTTGCTGTTGCTGAGGTAAGAACGTTGTTGGAAGACAAAGTCTGTGGCTTG
WI-18932d	177 C T ---	---	CTTGGTATTTGTTTAAATCCCTGTACATATCTTTGAGTTCAG/CJCTTTAGTACGTTGGCTGTTGCTGTTGCTGAGGTAAGAACGTTGTTGGAAGACAAAGTCTGTGGCTTG

WI-19042	193 A C ...	---	---	TTTGTGAGTGTGCTCTGCAATGCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGTG GATAAGGGAATAAGGCCACAGAGGTGAACTTTGTGCTCAAGGACATTGGTGAAGTCCACAG ACACAATTATCTCGACAGAACTTCAGCATTGTAATTATGTAATACTCTAACCAACGAGCTG TGTTAGATTGTAATACTATCTCTTGGACTTCTGAAGAGACCCTCAAT
WI-18984	208 A C ...	---	---	ATTGGCCCTGTACAGTTTGTCTTATTATTAATTCATTAACACTACAGGTGTGAATGGTTAAAA TGAGCCCTCAGTTCATTTCAGTTATTTCTGAGTTCAGACAGCTATTTGCACTGTATTAAAT GTAACCTATTAAATGAATCAGAAGCAGTAGACAGATGTTGGTCAATACAAATATTGTGATGCATT TATCTTACATATAAATGCTAAATGICAAITTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ...	---	---	GCTTCAATTGGCGATTGATTCAGTGCCCACTTAACACAGGTTGGTAGTGTACTCACTTTTGAAT ATACCTTTTCTTATTTGTAATTTGTAATATAGGATCCTGGAAATGAGACCTTGTGGAA
WI-18821b	76 T C ...	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAACTGTCTAGGAGCCCTCTCTCGAGGOC ACAGAGGCTGCGGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAACTTGCCAACTTCGTGTGACG GTGCTGTGT
WI-18821a	69 C T ...	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAACTGTCTAGGAGCCCTCTCTCGAGGOC ACATGAGGCTGCGGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAACTTGCCAACTTCGTGTGACG GTGCTGTGT
WI-19021a	20 C G ...	---	---	ACTCCTCTGCTGTGCTCCATGAGTGTCTTTGAACCAAGGAAAGTCACAGATTTAAAGAGAA GCAATTAACATCCTGATCGGGAACAAAGGTTTATCTAATAAGTGTCTCTTCCATCAGCTTG CTACCTTACCCACACTTCCCTCTGATTTGCGTGAGGAGTGCGCATCTCTACTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGCTC
WI-18908	70 G C ...	---	---	TGGAATTCCTTCATCTGGAAACCATCAGAAACCCCTCACACTGGGACTTGCAAAAAGGGTCACTA TGGTGTAGGGAAACATTCCATCCTTGAGTCAAAAATCTCAATCTTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ...	---	---	CACGGTCTCTGCATGTTACAGAGGCGCTTCTGGTCTAGCCACGCCCTGTATGACCGGCAATA TCCCCAAAGCTTTTGGGCTCCTCAAGTCATGCCCGAATTTAGATGTGTTCTTTCTGGAGAGGGTCT CCCTCCCTTACGAAACACAAAGAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCGAGGCACTGGGGGTGAAGTGTGCTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ...	---	---	CACGGTCTCTGCATGTTACAGAGGCGCTTCTGGTCTAGCCACGCCCTGTATGACCGGCAAA ATATCCCAAAGCTTTTGGGCTCCTCAAGTCATGCCCGAATTTAGATGTGTTCTTTCTGGAGAGGG GTCCCTCCCTTACGAAACACAAAGAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCGAGGCACTGGGGGTGAAGTGTGCTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ...	---	---	TTGAGGAGGTGGGTGAACCTCTCTTGCAGGGGATTGTGACACTGCAATTCCTGGCTGTGTTCQT/ CPGGGCTCTCTGAGACCTTGCAACGTTGATACAGGCCATGTGCCATGGTATTGGGCTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G	AGGCTGTGGCTTATGTCAACCAACAGAGGGTCTGAGAAGTCTGGGATGGGCTGGGATGGCCCTGGCCCTGGCCCTGGAGCCCTGCTGGAGAGGCTCTGAGAGATGAGTGGGCTGGGGAAGCAGAGTGGCTTGGTGGCCATGGAGCCCTGCTCTGCTCC
WI-19016b	184 C A	AGATGTGCTTGGCTTGAGCAGACAGACAGTCAAGTGAATGCTCTGGGCCA GTTTGCAACCAACATGTGCTCTTTTCAGTCAITTCACCTGTTTAAATATGACATGGTAGAGAAATAG GTTTATGGCAGTAATTTTGTAAATGTGTATTAACGAAGTTCAAGATTAGAAATACATCTGTGT CTGAAACCTTTAGATACATACAGCCGACCTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTGGGGCTGGATAGTCTCTGTTTGGGGGTTTGTCTGTGGCACTGTAG GTTTGCAACCAACATGTGCTCTTTTCAGTCAITTCACCTGTTTAAATATGACATGGTAGAGAAATAG GTTTATGGCAGTAATTTTGTAAATGTGTATTAACGAAGTTCAAGATTAGAAATACATCTGTGT CTGAAACCTTTAGATACATACAGCCGACCTGTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTGGGGCTGGATAGTCTCTGTTTGGGGGTTTGTCTGTGGCACTGTAG GGTTTGGGGCAATTTTCTGATAGAGACTGGCAAGCTTGGGCTAAGGACACCCGCCCTC ACCTCATCTAGAAACAATCTCTGCGCCAGACTTG
WI-19016a	161 C T	TGGGCAATTTTAAACCAACAGGCAAAATATACATATACCTGAATATAGGTAACCTCAAGCCATG AGTAAAGATTAGGAGTACTTTTATTTGAACAGGAAGTGGCATAAGCAACTCAGTGTGTGCC CTTAGGGTGGGAGCTCTTCCGACCTACCACTCCCAACCCCAAGGATCATTTTGGGAGAAAAA GTGCTCTCTATCTGGCTAGCTGTGTATCTAGGGAITGCACTTCTTACACGG TGGGCAATTTTAAACCAACAGGCAAAATATACATATACCTGAAT/ATTAAGGTAACCTCAAGC CATGATAGTAAAGATTAGGAGTACTTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTTCCCTACCACTCCCAACCCCAAGGATCATTTTGGGAGAAAAA GTGCTCTCTATCTGGCTAGCTGTGTATCTAGGGAITGCACTTCTTACACGG TCCTCCAGCTCTGTCATCCTGCTTGGGGTCTGTTTCAAGGCTCCAGGCTCCAGGCTGTTTCTTCAT TTAGGTAGGAACAAGGCAAAAGGCAAAACATACAGCCAGCTCTAGAGGCTCCAG/ATCAGAA CTGACCTTTAACTACAAAGGAATCTTGGATGAATTTTATAGCGGGCTTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCCCAATGTCTCCCTCCCGGGGG CTCTCCCTTAGGAGCTTGGCCCTTGCAGCCCATTCAGAGGATGAAGTCAAGCAATGAGT GGAGCTCATGCCCTCCATGAGGAGCCCTTAGTATGCTGACATGCTCCCTTATCTGCTCTCTCT CCCCAGTCTGTACACTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGGAGCTCTTGTAGAC GGAAAGGAGGGCGGTCTTGTGATGGCTGCTGGCTCTCTGGCTT GACGTGGACAAGGAGGTTTAAATGAATCTTTGTTTGT/CTC/ATGTTCAAAAAAGAGATTAA ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATA GGCTATTTGCCACCCACTCTTGGGCAATTCGCAATTTCTGGGCTCAAGTGGAGGCCAGGTG GGAAACAGGGCTCAGAAACAAAGGACATGCGCTCCTGAGCCAGTTCTCT
WI-20096	21 T C	
WI-19591b	156 C A	
WI-19591a	45 T A	
WI-20310	125 G A	
WI-20860	224 G A	
WI-19359a	39 T C	

WI-19766b	93	A G ...	---	TGGCCTCAATGACTGGTACATTGGAGAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGAGGCGAGG AGATGAACCATAGGAGCCAAAGTCTGACAAACAGAGAGGACACCAAGCCTGAACCCCTC CGGACACAGCAGAGTTACAGCTAGGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCTTCCTCACCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31	G A ...	---	TGGCCTCAATGACTGGTACATTGGAGAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGAGGCG AGGAGATGAACCATAGGAGCCAAAGTCTAGACAAACAGAGAGGACACCAAGCCTGAACCCCTC CGGACACAGCAGAGTTACAGCTAGGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTC ACCTTCCTCACCCTCCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126	C G ...	---	CTTCCTCTGTTTGGCTTTGCTATTGTGCGATTGGAAAAACCATTTGGAAGAGGGACTTTCTCTGCAA AACTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCACTGGAGCCCTTGACTGAC/GAAGC TTAGAAAGGAACCTGAAATTGCTTCTTTGAATATGATTTAGGCGGGCGTGGTGGCTCACGCT TATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACTGA
WI-20512c	59	T G ...	---	CTTCCTCTGTTTGGCTTTGCTATTGTGCGATTGGAAAAACCATTTGGAAGAGGGACTTTGTCCTG CAAACTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCACTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAACCTGAAATTGCTTCTTTGAATATGATTTAGGCGGGCGTGGTGGCTCACGCT TATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACTGA
WI-19599	230	C G ...	---	GGGCTTAAATTCCTCTGTTTGGGACTGGTCTCCAGTTTACAGCAAGGATCGACCCCTTTTC ATAACCTTCTACATTGGAAGAGCACACCTTGTATACAGAATGGCTCCGGAAGTCTTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGCTGATTTGGCTCACACGTAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGCGAC/GTTCCAGAGTAACACTGCTA
WI-20679	82	T C ...	---	TGTTTGAATAAAATTTCCATGGTCTTAATTGAACCTGTATGTTACTTTCTTTTGAATATCCTTTT TTCAATTAATAATTTCTTAAACCACTCTATGTGTTCAACCTCTGTTTAACTAAGATATGGGT TTTGGAAAGGCCAACAGTCACCACTCCAGCTCCAGTGGGCGAATGGTCTGTTTGGAAAGCTCTC CAGGTGTTTCTCCAGAA
WI-19909a	29	T C ...	---	CCAGAAATAAGGCTGAATATCTCTTTCT/CJTAAATAATAATTTTCTCTTTGCTCTTCCAA GTAATCTTAAATGAACCTGTTCTAGTCTATTTTAACTAGGCAATTAACACTACCTAGGCGGG TTTTCTCTTTTACCTTGTCTGACTGTGAATCAACTAA
WI-20341	221	G C ...	---	TTGAGAGCTGAGAGAGGCTGTGAGACATTGTAATAGTCTTAGGGGCTAGACATTAGGAAG GCCAATTTATGATTAAGTAAGATGTGAGGCTGATGAGAACTACTGCTCCCATTTGTTAGCAGGA GGCAGGAAGATGATCTGGGCTCTCTGGCAGCAAAAGCGTGTGGTAAATAATTTGGGTGACGTATGC ATCCCCCATGCTATGGTTTGGTATGCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60	T C ...	---			TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATAGTGTCJGGA AACAGTAAAGCAAAATACACACAATTAGGAGAAATATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAAATCTATTCCATAACCAGGTAGATAATGTGACA GCTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCGTATT
WI-20895	107	G C ...	---			TGATGGAAAGTACAAAGGCTCTGAAGAAGACAGAGTAACAGAGCGCAGCGGTGTGGC CACTCCACAGGAGCAACACTTGACTTTCATTAAAGGCAAGGCTTTTACTCTGTACTTTTCTC CCACATAGTTTAAACCCAAATAGAAAGGCATTCTATCTCACACTACTGCTCTAAGGTCTTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C ...	---			CCTGCAATCACAAAGTGGAAGTGAAGTATTTTGAATCATACTGTTTAAACCACCTTCAGAAA TTCATATCAAAACACTAGCAACTCTCTCTTTATCAGA
WI-19415c	161	A G ...	---			CTGGATTTTAAATTTCTGGCCTAATACCAAGTGAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCAGAGATTCCTTAAGTAAGTATTAAGCACTAGAGCTAGTCCGGCAA GTCAATGAGACCTTAGCTGATCTCAATAGAGTCCACCTCATGAAGGAGATGATTCACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T ...	---			GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACTTCTG GCGTGCATGATGAAGAGACTGTTGGTCAATGGCGGTGAATGTCCTCTCCAGGCTCATATGATGTCCT CGAGTTGCACAGGGAACTGCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98	G A ...	---			GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACTTCTG GCGTGCATGATGAAGAGACTGTTGGTCAATGGCGGTGAATGTCCTCTCCAGGCTCATATGATGTCCT CGAGTTGCACAGGGAACTGCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98	A T ...	---			ATTAGTCTGTTGGGCCACATCAAGGCCATCCACACAGCTTCTGTAGGCCATTTGTAACACAATG TTAAAGGTACAGTAAATAATACAGTATTAATATCTTATTTGTAGCAGCGGTGTAGGCTCATTT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGCTGAAAGAACTTTGCTTT T
WI-19641a	46	A G ...	---			TCCAAATTTTCAGAAACATGTTCCATGTTTATTTGTGATAAGCACTAGTATATATAGTCTCATGTTT TTAAATTTATGAATAACGCTGTGATTCATTTGATTTTATTTACAGAGATGTCCAGGCTATCTCATTC AGTTATTAATAATGGATCAGATAGTAAGTCAAGATAAGTGCATAATGTGGTTTAAATTTTAA AATACTCAGAAATGAGGTAGTATTTTAAATTTTATTCATCCACCCACCTTG
WI-19642b	52	C A ...	---			ATATAGTACCATCCATGTTTCAAGCATGGCTGGACACATATCCCTTC/AGSGTAAACCCAG GACTATGCATGACATCTTTAATACGTATTTTGTGAGCAACAGTTTTCATGCTATTA
WI-19673b	180	C T ...	---			TCTGCCATGATCAGATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACTTCTGTGTCATTGCCCT TACTCTCAGTGAAGTGTGCTAGTGGATTACCTACCCCTGCTTTGATCACCAGCTGTAATCTAATAGT GAAAAGGCAATGATGCTCAGTATCATCTGTGAAAACATTTTCTGCTTGGACAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCATAAAACACAGCCC

WI-19066e	147	GC	---			TGACAAGGGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGCTTAGCCAGTCCAAATCTCTACGAGGAATGG CATATGTTCTTGCGCGCTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGATGCTCAATTAC AGTACCATTGCAAGGCAAACTTTTCTTAAGGCCCTTCACTAGTTCTTTTAA
WI-19066c	100	GA	---	---		TGACAAGGGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCG/ATCCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGATGCTCAATTAC AGTACCATTGCAAGGCAAACTTTTCTTAAGGCCCTTCACTAGTTCTTTTAA
WI-19066b	87	CT	---	---		TGACAAGGGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAAC/CTTCAAGCTGATCGCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGATGCTCAATTAC AGTACCATTGCAAGGCAAACTTTTCTTAAGGCCCTTCACTAGTTCTTTTAA
WI-19066a	72	CT	---	---		TGACAAGGGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAAGCTGATCGCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGATGCTCAATTAC AGTACCATTGCAAGGCAAACTTTTCTTAAGGCCCTTCACTAGTTCTTTTAA
WI-20660	105	GC	---	---		TTTACAGCGAGTTTTCCTCGTCTCAATAAGTATGAATCTAATAGATTAGGGTGAAGAAATGTG TGTCTAAATAAATCTCCCTTTTGAATGATATTTGTG/TTAATAAGGGGAAGCAATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTATTCATTAATCTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCGCCGCCCAAAATACTGTTTAAACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCCAAGATGGGGTCTCTTGGCAGGCTTCCCTCAGTCTTCC TCCACCGGCTCTCTCCCTCCAGGCTGCTGATGATGTCACCCCTTGGTGTTCGCTCCATGCCC TTGAAAGCTCTGAA
WI-18768	120	CT	---	---		TTCCCCAGGGTCTGTATTGCAAGTAAAGCTCAATGTATTAATTAATCTAGTTGCTCTTGTCTTTG GTCTTCTTCCAAATGATGCTTACTACAGAAAGCAAAATCAGACACAATTAGAGAGGCTTTTCCATAAA GTGTAATTTTAAATGCGTGAACCGGCAACCTGTAACTGCCCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTCTCTATCTGTGATCTACCTGCTCC
WI-18790	49	AT	---	---		GAAAGCCAGAGATTAGCCCGCATTCGGCATCTGTCAACAGGAGACAGAA/ATGTCATGGACAAGGGA TGAGCTTTACAAGATGATGCACCTTTGGAGATCAGAAAATTCATATTAAGCAAGTGATACAAACA CAGTGATTGGGAATGCT
WI-18987	35	GA	---	---		AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC/G/AGTGGCCAAAGCCACACTACCCACCTT CCCCAGTGGCCCCGTGGATCCTGCTAGCTGGACAGGATTCAGAAAGACACCGGCTGCACA GAAAGAGCCAGATGAGCTGAGTGTGGTCAAGCCCCCTTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA

WI-19236	54	GA	---			TACACAGAGGTGGACCTCTGAGGCTGGGTGGAGGGGGAAGGGA/GATGGAGAC CTGCTCCCGAGCTCTCTGTGACCGGTTTACATGGGAACAGGTTTACATCTGTGTTAGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGTACACTCTCTGGCTATCTCAGGGGAATGGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGGAGGAGTCTGTGTGTATGTATACT
WI-19144	222	GC	---			GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATCAGCCTTCTGACTCCAGCCTTCTTAAGG CTCAGCCCAAGGAGCTCTGTGGCTGCCAGCTTGTGAGCTATCTATCTATTTCAATGACAA ACAGGAGAACCCCTTTTCAGGAGTTTCACAGGAGGCTGTAGCCAGGAACCCCTCTCTCTCTGGT CTGGCTCTGCTGGAGCGGGTGTGGGAACCAACACCTTCAGTCTGGTG
WI-19139b	110	CA	---			CCGCTTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCTGACAGAGAGTGGGTTGGCAGACAAACACTAGCA/ATTTTACAGGGGTGTGGCAG ATGGGTGTGGCACTGGAGCTGTGCAGCATGTGGCGCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAATCTGGCTGTGGAGGCTTTGAAG
WI-19139a	66	CT	---			CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA CTGGCAGATGCTGACAGAGAGTGGGTTGGCAGACAAACACTAGCA/ATTTTACAGGGGTGTGGCAG ATGGGTGTGGCACTGGAGCTGTGCAGCATGTGGCGCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAATCTGGCTGTGGAGGCTTTGAAG
WI-18910	112	TC	---			GGCTGGGACCTTTAGGAAGTGAATGCAGGTGAGAAGAACCTTAACATGAAAGGAAAGGGTGCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTGTGTCGGCTCATGTGGCAGAGCAT CAGTGGCCACGGTTTAGG
WI-19235	173	AG	---			TTCAAGGAGGTGGAGTTGTGTCAGCTCTCTGCTGTGATGTGGAGCTTCTGTATTTGAAGAAACA CGAATGCTCTGTAGCTCTCTCTTCTACCTGCCAGTATGCTGTGTATTTACAGCATGCCCTCTGT CACTCATGCTTGCCTAATTTGTTCAAAATGGTGAAGAGGCTTCATGTAAATATGATCAGGACCCACC TCCAGTCTCTGAAAGTGTGACAGTGTCCAGCCGGTCTGCGACACTA
WI-19222	179	CT	---			CGTTTTCCCTAACTACCCAGTTTAGTTGGGATGATTTGATTTCTGTTGTTGATCCCTTTCTAA CTTGAAATTTGAGCCCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCGCCACCCAGGAAGT GGCAGCATCCCTCTCTCCCTAAAGGAGCTCTGCGGAAC/TTTTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGTACACTGACGTGTCCAGAAAGCAGCACTTT
WI-19117	134	AG	---			AAATAATGCAAGCAGGAGGAGAAAGAAATGCACCTAAGACAAGCACTTCTCTATAGAACAATTG ATCTGTTTTACAGGAACAAACCTTGCCTTTGAATTTACAGAGTACAGCTGTACATAATGTCATGAA A/AGTATGCTATTTTTTCTTAAGACATTTTTCATTCAGTAATTTTCAAGTTTTTCATACATGTACA CATTTCTAAACACATGATACACAGCAGCACTGAAATGAATGCCGAATTTG

WI- 20561b	94 T C ---	---	CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAGCAGTTTGAGCAACACTGAITGTGCTATTG TACTTCAGATGAAAAATCCTTACATGT/CJGGAATCAATGTCTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---	---	CGTTGCTATTAAAGATGGCTGTTT/JGJTAAGTATAAGCAGTTTGAGCAACACTGAITGTGCTATT TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---	---	GCCTTCATTTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCTTCAATATATGGCGTTAGAACAT AT/ATATAAATCTATATCATATATTTATACACACAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20116c	59 T A ---	---	GCCTTCATTTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCTTCAATATATGGCGTTAGAA CATATAAATCTATATCATATATTTATACACACAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20116a	22 C G ---	---	GCCTTCATTTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCTTCAATATATGGCGTTAGAA CATATAAATCTATATCATATATTTATACACACAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20466b	133 G A ---	---	AAAGATTTGCAGTCTGGGACACAGTTTGGAAACACTATTTAAGGTTGCACATATTACAAACAG NTCCAAATGGTGAACCTGGTATTCTAAGATGAAGCTTAATGAACATAATGAAGTGAATAAACGCT G/ATGTGAACTAATGTTTAAAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAT ACAGTAACACTACTTTTATTTCTTTTGTCTTTTATCCCTTTCAGGTTTCGATT
WI-21444	39 A G ---	---	CTGGGACGCAAGTAACCAATTTAAAGAAATCTCTCAAC/JGJAGTCTCTTTTATGGGTAATTCOA GTTGTTACAAAGTTAAATTAATCTTATGGAACCTAATCTTTGTTATTTATTCGAGGAAGAAATCT ATAAGATTGACTTACTCATGTTGACTGGTITTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---	---	AGAATGGACAAATGATGAGATGTTGTGAGCATTTTGTAGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTTGTAACATGCTTATCTAGCTAACCTAATCTTTTGTAGAAATTAAGTGTGCTGG GAGATTGGATAGAT/CJGCTAACCTATCTCAATTTTAAATTAAGTAATGTGAGCAA
WI- 22091c	205 G A ---	---	GGCGTGTATTTGATGCAATGTCCAAACAGTCAAGTATCATTTGAATCCAAATTTCCAGTAGAG ACATGACAGGAATGTCAATGTAAACATACAAGCATATTAACCTCCCTTAAAGTACTCAATTTTC ATTACTGTGTCTAGCTTTTAAAGGTTTAAAGGTTTAAAGTGTGTAGCATTAAGTGTATTACTTGAGGGCA ACA/G/AAATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG

WI-21609a	42	CT	---	TCATGAATATGACGCTCCATAATCTCTCCCTTTGAACAAAC/GTGTGAGATCCGTTTCAACAGCTGT AAAAAAGCCCAACCCACATCAACAGGACAGACAGTGGCAGTGAAGAGGAGGAGCTGT AAGGATGTTCAAAGGAGGCTCCCGCTATGTGCCACTGGATGTAGCAGTGAAGCTGAGTGAGTGCAGGC TTTCGGCTCGGAAGTGGCAGAGGCTGAGACANTGCCAAGAGAGAGTGGAG
WI-22512a	104	TG	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCTAAATCCCTTGGTGGCTCCCTAGGGCTTCA GGGTAGCCCTGACATCATGTGCTCTTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTTAAGGGCAGGCAGCTACACTTGACTGA
WI-21208b	139	AG	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGAGTATGTGACAG TTTC/GJGTGACTGGTACAGAACACACAGGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAAT CTACGG
WI-21208a	121	AC	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGAGTATGTGACAG GGGTTTCATGCTGCTGACAGAACACACAGGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAATC TACGG
WI-18829d	58	AG	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACATTATGTGACTCTTGT/GJGTTTCA TCATACAGACACAGCACAAAAAGCACCACCCATGCTGTGAGGAACATTGGACCATTGCACCCCTTGA AA
WI-18829b	35	TA	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGTTAAATTAACATTATGTGACTCTTGTGATTTC TCATACAGACACAGCACAAAAAGCACCACCCATGCTGTGAGGAACATTGGACCATTGCACCCCTTGA AA
WI-20964	87	GA	---	AGCCAACTCAAGGCCAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAAATAG/AGACACAAAGAACCTCAAGCTGTGAGGTCAATTTGTATTA AAGAACTAAGATTAGTAGAACACACACTAGAAATCTCTAGGAGAGCTGAAAAAGAGGAAC AGATGTTAACAAAAATTAAAGGCTGCTGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59	TA	---	CTCTGAACCTAAGGGCGGTGAAGGCATGATTGTTTTGGCACACAGAGTGGATAACCATTAACAT TGGCTGGAATGAGGTGGTGCAGAAAAATAAANTGCACAAATCTAAACCACTGTTGAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATCACTCTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCTTAGGT
WI-22130b	165	CT	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCTTCCCTCTCTCTGACAC CAGCAAGGGGAGGCACCATCATCCGGCCCTGCCCATCATGCATCATGATGATTACTAGCATTAGGA GCCAACGGAAAGGACCCCGGCTTCTCT/GTGTGTTTAAATCCAGGTTAAGCTATACACGTTAA ATACATGTCGGAGTTACATGGTCTCATGTCAGTCCCTGTGTGATGGGAATGAC

WI-21661	117	GC	---			GCCTAGTCTCCACCCCTTTAAATGTACTAGGTACAAAATAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATA(G/C)TTTAAATGTCACAGTC ACACAAAACCTACCTTCTAAGGAAAACCTGTCAGTGAAGCGGTTAAATTTGCTTTTACGCTATGAAG GA
WI-21980a	25	TC	---			TCAGTTTAAACACATTCATCAAGGAT(C)AGATTAAATTAATGTCAAGTGAGCATAAAAGGGAGATT TAAACAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21638	71	AG	---			TGCTGTATTAAATGTGGTGTTCATTATCTTATTCACAGATGGAACAGAAAATACCAGCTTTT AAA(G)GTAGCAATATCTATTATTAATAAATAATTGAAATAACACCATAATAATATCAGTAAGGA AGTAATCTAATTTGTTGTTTTCAGAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAACTGAAGGTGTAGAAAACCTAGGAAGGGACAGGGATTTC
WI-22457a	112	GA	---			TTGCTATAATTTCTTAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCATCAGTCAATTAGA CAAACAGTAAACATCTGGACACGGTTTCAGGCGATGAAGGATACAG(CA)CAGTTAATTAACATAAAG GAACAGAGTCCCTGCAATCTGAGCATAGGATGGGGAACAGTAATGCAGATTAACTGCGGCC AAAACCCACTGAACCTACCCACGCTGAAAACACTGAAGGATACCTGGGTAAGGA
WI-21524b	97	CT	---			GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCCTGATGTACGACCTTCGCGTCATCTTAT AATGGTTAATAACAGCATTCCTGTCTACCC(C)TGATGATGCTTCTCTCTGCAATGGAGCTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCGACTTTCTCCAAAGTTACTTCTTCCAGGGGATG
WI-21524a	35	AC	---			GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCCTGATGTACGACCTTCGCGTCATCT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTGCAATGGAGCTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCGACTTTCTCCAAAGTTACTTCTTCCAGGGGATG
WI-22652a	32	GT	---			TTACCTTCCAAACCCAGGCCACTTTGGAGAAAG(G)TAAGAGAAATGCTATTATTAATTAAGCCAAAGAC AATAGGAGCTACTGGGGTAGAACCAAGATGGGCGATGCCATACACCATCATCTCTGCCACAGAACCC TTTGACATGCTGCOCTCOCTACTCCGCACTACCTGCTAAATGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197	AG	---			CAACAGGCTCATGAAACAGAGCCTAGGATCCAGAGCATAGGAGGTGGTGGTGGGAGGGCTC TGATCCCTTTCTCAGCAGACACCATCTTACCCCTCCCTGGGAAAGCAGCATTTGGAGCCCTACACCA CTTGTCCTTTCTCAGCAGGGTAAGAAATGCGAGTATTTCAGAGGGGAGGTGAGCTGGGAA(G)G TGGCAGAGCAGCAGCTAGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG

WI-22724	117	A G ---				TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGAAGTGTGTTAGAGATATAGGA CAAAATCAAGATTGTCAAAATGTATAGTAACCTGTTAAAGCTTGCTAAGGGT[AG]GTATTATCTATTTT TGGGATATGTTTGGGAAT
WI-22750	48	G A ---				TGTAACCTGTGTTTCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAA[AG]AGGCTCATACAAGGT TTGGAAGACCCATCTGACTACTAAGGAGAGTCAGCATCTGACCATTCTGACTGTGCT
WI-22775a	60	A G ---				TGCTGTTCTTTAGTTCATGACGTTTATCAATGTGTCTACTGTTTCCATTGTTTACATCA/GTGTGA GGAAAGGGAATAAATACTCCCTAAAGGGGAGCAATAATTTCTGCTTTGATTCCTTCAATTCAGGCAAA TATTTGTGAGCACCAAGGGCCAGATGGGAAGTGGGATGTAGGTGTGGGAGCCAGGAAGGAAG GGT
WI-22808	143	C T ---				CTTAGCTAATGAAGTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAGTCTGAGGGAG CCTAGTCTCTCTAAATGAGACAATGTACCCATGACAAGGGCTACAGCTTGCTTTAGCAACCAGGA GGATGAAGAC[CT]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCTCTGCTGCTTGAGCCCTCATCCACCCCTCCAAAGCCCTCATGCCACACACCGTGTCCACATT CCCCATCCTCCCTGCTGCTCCCATCTCAAGTCCCAATCCAAAGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAGAGGAGGGAGTGGAGATGGCAGAGATGGGGTGGAGCCAGTGGCTGTGGGTC CT[GA]TTGGCGTGGTGTATGTGGGGCCCATCTGAGGCCAGAGTTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTGACATGTGG[CT]CTCTGGTCCCATTTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGAGCCGAGAAAAACACACACA
WI-21314	122	A T ---				CCATATCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATCTTTATCACTAT GACTTTTCATTTGATTTTATTGTTTCTTCCATTCTCTGCAAACTTTTC[AT]TTTGTATTATAA ACTGTTTCTAAACTTCACTTAATCTCTATCTGTATTCTGTTAGTTCCTGAACTTCTTTTAGAGG
WI-21186	95	G A ---				AGCGAGCATCAGAAATCACCTAGAGGGTGAATAACAGACTCTGGACCCACCCAGAGCTTCT GATTCAGTAGGCTGAGTGGGCTTAC[GA]AATAGTATTTCGAAGACCTTCTTAAGTGTGTCAG ATGCTGTTTGCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTCTTTTAA GGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGTTATGTAAT
WI-21187a	94	A G ---				CCACGATACTATAAAGAGAAAAATTAGCTTTGAAAAACAATAACATATTTAGTAACACACACTT CATTTTATAAACACACATAAAGACAC[AG]GGNTCTCAGTAATCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAAGCCCATTTGCATCACTAGGGGAATTCCTAAATGCAGATTCTCAGGCC CTAOCCTACTGACTACTGAATCAGAAACTCTGAGGGTGGAGCCAGCAACCTGT

WI-21190	39	T C	TTTCCCCACATACCAATGCACCTGTTTGTATAAACTATTCJGTGGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATTAACAATAATTAATAAATCTGTACTATTACTGC TTAGTTATCTAGTGTTATTGAGAAAGGAGAGTCAGCATAGTTTATTTTCCATGTATAAAAGCTT AACACA
WI-19937d	186	G A	ACCATGTGCATTTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAACTTGGAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTATGATGGTGTGTTCTCAGCAAGTCTGATJCCAAACCTTC CAAAAAGAGCAGTCATTGAAAATGCTGACTTATGCATTGCCCTCAGGAAGAA
WI-19937c	185	C T	ACCATGTGCATTTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAACTTGGAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTATGATGGTGTGTTCTCAGCAAGTCTGATJCCAAACCTTC CAAAAAGAGCAGTCATTGAAAATGCTGACTTATGCATTGCCCTCAGGAAGAA
WI-21117b	227	C T	GAAACGGGGTCTAAACAAGAAAGTCTCAGATCCCACTGAAATCTGTTTCAGTTTCACAGGCTC TCTCAGAAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTCTGGGG TCCAATCACATACTTCAGGTTTCAGACTCCTAGTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTATTTCTTTCTACTGAAATCTTGGGTGGAG
WI-21122a	42	C T	TCACTTTGTATCAATCCCTGTAAAGCTAAAGTTATTCACJTTTAAAGGAACCTCTGTTTTTC TTATCAATGTACAAAGCCTGACGGCTTACTGTACATATTGCTAGCAGGAGACAACCTGGAATACT AAACAATACTGGAATTCACATTCACAGACAGCAAGCAACCAACATGGGATGCCACACATAACTTCT TTGTAGGTTTTCACAGAGAGCCTATTGTTGGGTTGCT
WI-21254	53	A G	CAGTTTGTACAGGAAGGCCCCATGAATGTGGGCGGAACCTATTCACAGGAGJAGJCAAGGAGAAG CTGTCTCTGG
WI-21054	23	G T	AAGGAACTGCATGGGTACAAATGTJTTCCAATTCATATCTTAAAGGTGGGGAACGGGTCTATCT TGGCTCTCAGAACAGGGGGGAGTCTATGCACTCTCTG
WI-21059b	181	T C	GGACACAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCATTTCCAGCTTCGTACACATCTTAATTTCAAGCTGAAA AATCTGGGGGAAGACATCTTCACTGAAGTCATTTCTCTATTTCTJATTTGAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTJAGGGTACTATCTCTGCTAAT
WI-21059a	63	C T	GGGACACGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGJCTT GAACACAGCTGCCAGCATTTCTGGGCTTGCATTTCCAGCTTCGTACACATCTTAATTTCAAGCTG AAAAATCTGGGGAAGACATCTTCACTGAAGTCATTTCTCTATTTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTJAGGGTACTATCTCTGCTAAT

WI-20442	37 T C ---	---	TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAGTGCAGTGAAGACGAA CA
WI-21235	43 T C ---	---	GTGACAAGAGGTGAAGCAAGGACAAAGGGGACAGGGCAGTCT/CJCTGGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---	---	ATCAGAACTGCAATCTGCACATGAAGAAGCTGGGGGAATGCTACATCTGGAAATTT/CJCATTAAC ATCAACGTAAATTTGTCCGACCAAGTCTTCATTCGCTGATCAGTCTTTTGATATAGACAGATCCAAACAT GAACTCCTGAAGCAAAATGAATATTACCTTGTGCTTTTCATGCCAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTTGACAGGGATCTTCT
WI-21149a	167 G A ---	---	AGGACCTGCTCTACACGTTCCCTACCCACCAGCTTTTGGCAAGATAGTTGACTAAATACCACCT AAATAGTGGCTTTTCTTTTAAACAATGACCTTATTTTATCTTTTAACTTAACTGAGTCTTTATATA CAGACCTGCCCAACTGGAAAGCTTTTACACGATGCTTCAGATGCGGCAGTATGACACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAAACCCAGGCTCTACCTG
WI-21376b	188 A G ---	---	GGTGCAACTTGGAAATATGGTTTAAACACAGGATAAGCATTAAGGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/A/GJBAAGTATCT GAACTGAGCACGCACTCATGCTGCAATGGGAACTCTGGGGAGAGAGCCT
WI-21382d	125 C G ---	---	CCATTGCAGTCCAGAGATGAGAACTGGACCAAGGCAATCATGAACAGACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAAGTGGGGCGGGTTTGGATCCAGTGGGATNGGCTTCCQ/CJGAGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCAGCTCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201 G A ---	---	TCCCTGAGGTTGGAGTCTAGCATAGTCCCTCCCTCAAGAGGGACAAGGGGTGAGGGGACAGC AAAAATCCAGTCTGCTTCAACCAAGGAGACTGCCCTTTGGGATGAAAGTTTCTGAGCTCCCTCCATT CTATTCTGTGGGGCAGCAACATGCCAGGGCTGCTGTTAAATGGCAGGGTCACTTTACCGGGGCG /A/CAGGCTAGTGTGGGCTGCTGCTGCTGGGGCCACCTGGGAACAGT
WI-21202b	156 A C ---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTCTGTATAAGCTAAATATGTC/JTGA GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTTAACTGATTTATGAGGG AGGAGGAGAGAGTTGACCA/A/CJGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTCTGTATAAGCTAAATATGTC/JTGA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTTAACTGATTTATGGA GGGAGGAGGAGAGAGTTGACAAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	GCATGAAAGAACTCCAAATCAGACTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTGATCAACTTGGTAGTACCTCATATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTCGAAAGTGCCAAAGTCATTAATTAACCAATTTTACATAATTTGTAGG GACAGTACTAATCTACATAAATAAGGGTTTAAAAATGTTGTTGCTTA
WI-21627a	106 A G ---	---	GCATGAAAGAACTCCAAATCAGACTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTGATCAACTTGGTAGTACCTCATATGGATATTTATGCTAGGAATGA CAACAGTAGGGCATTCGAAATCCAAAGTCATCTAATATAAACCAATTTTACATAATTTGTAGG GACAGTACTAATCTACATAAATAAGGGTTTAAAAATGTTGTTGCTTA
WI-21399a	75 C T ---	---	GGATTTGAGTCCCAACTTGATCTCAAATTCACCTCTTGCAATGTAACCAAGCTCATTCCTCTCAAAGTT TCAGTTTCCTTCCACCAGTAAGGAAAGGTTGGACCAGACATGTGGACCGTAAATGCTTGTTGTA CTGCCTCTGCATTTCTCTGAGGTTGTGTCCCTAGGACTAGTAGGATCTCTCTGCTTCTGCTGCC TTAAGTAGGCATAGTGCTGATGACGGCTGAAGCCCAATTCATCATGTGT
WI-20320a	68 G A ---	---	CGATGCTCTGAAGTAGGAGGTTAATCTTTACATGGTGAGTGGGTACAGAGACAGACATCAAT CIGATTCGTGTAGCAGCAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGCTGGCTCTTAAACACAGTAAACCAATCAAAAGAAAGAAATTTAGAGGTTTCAGACATT AGGAACAANTGTGCCAGAGATACCAGAGCCCTTTGAAGGGGAAAGGCGTCACT
WI-21249	155 T C ---	---	TTTGCGCATTCAAATGTACATGTAAATCCAATTTAAGCACTCAAAATGTTACACTAAGTTTCAC TAGATCTAAGTATCCAAATCACAATGTATCTAAGTTTCACATTTAAGAAACAATTAAGAGGTAAT AAACTCTAGGTGTATACATTGATGGAAGTGTATTTATTCGTAATTAAGTCTGTTCAATTCGCGTA AAGTATGTTGTCCCAATTTACGCTGTTTAAAGAAATATAAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTCATGAATACTTTGAAGGGCCATTAGAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGACAAATTCAGTGGGGGACGCGGCTTGCGCTCCAGCTGGGTTTCC AGATGCAACAAATTCGCGGTTCTGGCTCTCCACTGGTGGGGATCGCGCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCAACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCACACTGGCCATGGTGGTGGTGT CTCTATGACCGAGGCCCTGAAACGGCGGGCAGGGGAGAGAAACGAGAACTGAGTCTGGGGGTG GGCAACAGCTTCAGACCCCTT
WI-21475a	181 A G ---	---	TAGCCCTCTCGCCAAACATCTGGCAATNTGAGGCTGGGGTGAGCAGTTGGCCTGATGTTGCCAGAGTAG GATGCTGATGCTGCCAGAGATAGGTGGGCTCCAAACCCAGGCTTCCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGACCTGGGACGTGGCGAGTCGCTCTTTGGAGAGGAGCAAGAAAGCCACAGCAGCAAC ACTTAGGAGCAGAACCCCTTCGCGTCTCCACCCTATTTCTCCCTCCCTGAAG

WI- 21475b	117	A T	---	TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGTGGGCTCCAAACCCAGGCTTCCTGCTCTACTAAGCA CAGCAGTCTGAAGCTTGGGACCTGGGAGTGGCTTTGGAGAGGGCAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCTCTCCGTTCTCCACCCCTATTCTCCCTCCCTGAAG
WI- 20893d	207	A G	---	TGTTTGTTCCAGCCACATCTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTCTGCAGGG CTGCTCTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTCATCAGCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAAT TTCAGJACATAACATTTGGTAGAGTAACACAAACACCAAGCCCTAAATG
WI- 20893c	179	T C	---	TGTTTGTTCCAGCCACATCTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTCTGCAGGG CTGCTCTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTCAGTAAAGTTCATCAGCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAAT AGTTTCAACATAACATTTGGTAGAGTAACACAAACACCAAGCCCTAAATG
WI- 19941c	71	C G	---	GAGCTCAAGGGGAGACCTTTACCCAGATAGGACTAAGTGGAGGGTGGAGGAAACCAAGGTGAAA GGTATTCGJGGTCTGTGTGAGACAAAGCAGGGGGGCTTGAGAACACAGAGCAAGGTGGGTTTGAG GGACACAGCAGGGTGCAGGAGGGAGATGGGGGACATTTCTTATCCAGTGCATGTCCCTTAAAT AACTGGGTACAGGAGCATTTNGAAGGAGAACCAAGGACAGAACGACAAAGCG
WI- 21552b	166	C A	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATAGATATTTTGTACAGATACACAAATGTG TAATAATTACTCAGAGTAATGCGATCTCTTCACTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTATCTCTGATTATTTAAATGTAC/AAATTAATTTATTTGAATTTAGTTACCC ATTGTGCTATCAAAATTCATCTTATCTCTTGTAACTATTATTGTGA
WI- 21552a	66	G A	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATAGATATTTTGTACAGATACACAAATGTG /AJTAATAATTACTCAGAGTAATGCGATCTCTTCACTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATCTCTGATTATTTAAATGTACAAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATCTCTTGTAACTATTATTGTGA
WI-21512	54	C G	---	TCCTGCTACTTCTGCTCCCTCCCTGCCCGCAGAACCTTACAAAATATTCTGTG/JTAGAGAGGA AAGAGCTGTGCTGCTCTCTGTGAGGCAAGCTCAGGTCCGGGAAAGGCACTGTGCTGTGATCTGTC TCAGTGTGGGAGGTCTCCACTCGCCCGCACAGGCGCTCGGGCCAGAGATGAGATATGCTGTAA TCCAGTACAGGGGCTGCGTCTGGGCTCCCGCAGAGCTCTCTTTGGGGG
WI- 21513b	192	G A	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACCTCTCTAAGGAGGCAAGCAACTTCCATT ATTCTTAGTTTAGACCAAGATCTTTAAATTTTATTTCTCTTTAACTGTCAAAATACACCAATA CTTAGAGGAAATATTACAGATATACCAAAACATTTTAAAGATAAGAGGCGAGTGAAG/JAGTAG TATTCTCTACATACCACAGTATACAATGATGCTTCTCTGAGGTTTAGGAAC

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WI-22082b	67	CT	---			CAGGACTTGGTTTGTGTCCTCCAACTGCACATAAATGTCCCTTTTGTGAGTATTGGTTGTGTGTC /TGTTCCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTTGTCTTATCCGGATGACGG AGGTACACGGGGCGCTCGCTCAGTTCGCCGGAAGGACGTATTCGCTGAAGTGGAGAGTCTACTC CTCCCCACAGGAGGCCACGATTTCAAATCCTCTTGTGCTGCAACTCT
WI-20993	139	A	G	---		AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTTAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTTCTTGTAAACAAAGTGTATACATTAAGACAGTATTGAGAAATGGCTTCAGGATTAATTTGA TTAATTTAGAGAGGCTTATTCAGGCTTCTAGCTCATCCACACATCACC
WI-21723b	125	A	G	---		AAGCGATTTTAAATTTGATTGGACATCTGTAGGTCAATTAATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTCAAAAGGTTAGTCATATTCGCCA/AGJCAACA GCATGATAAATAATCAACTATGTAGAAATAGAACTTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	G	A	---		AAGCGATTTTAAATTTGATTGGACATCTGTAGGTCAATTAATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTCAAAAGGTTAGTCATATTCGCCA/AGJCAACA GCATGATAAATAATCAACTATGTAGAAATAGAACTTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	T	G	---		CAACAGATGCTTGAGCCAAAAGCAACATAGCAGAAATACAAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTACTATCCTTTTGTCCCACTTCTCTAATCTCTTTGCCTTACAA TATATACCTTCTAGGTATCACTCATCTATAGGAATGCCCTCTAGTTAATGTCCTGCCCAACAA ATACTAACCCATGAAGGATACTATGGAACCTTTAAATGGACAGTGGG
WI-21006a	106	A	G	---		TGACAGATCACACCACATTTGTTGTAACCTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCCTTAAAGAACACATACACACATGTGCACACAC/AGJAGAGGCAAGTACAAAATGTAAACC CCACAAAAGTGCATGTGAATGAAAGTGCAAAAGGCTTCATTTGCAAACTCTGAGGATCATTTCTCT CTGCTCAGGAAATTAACAGAAAGGTTCTTAAGTCCCTAGGCT
WI-21761b	138	C	G	---		CTGAGGCTGCTCTAATCTAATNTGACGAGCGAGTTCTCGGCTTGGAAATAACTGAAAAGATTCTAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTACATCTCTCTGCTGCCAGTTAAACGTGCCGTGG CTGJCAATACACAAAGCAAGCGTAACCTTGGCTGCCCTCAGGAAGGCTGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	G	A	---		AATGAAATGCCACCCAGAGGTTAACAGCTTGCATGATGCAACTGTGGGCAAAATCAAGTTGT TTTAATACCAGTGTGACAGCTTGTATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTACATAA CTAGGCCACCTGAAATATCTGCTAGTGGG/AGJAAATTTACAAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGCAAT

WI-19891c	172 C G ---				TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATGCTTGGTGCCCTCCCTCCCGG ACTCTCTGTCTGGGAAAGCTGGCTTNGCTCCAGACACAGTGTCAAGATGCCAGCTCTCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGTCTGACTCAGCTGCTCCGCGGCGTGGGGCGCTGCTTGT CAGCGAGCGCGCGGGAAGGAAGGAAGGAGATCCAGGGTCTGCTG
WI-20155a	81 C T ---				GCACCTGTAGGGGTGTAGCTTCCATGGTTCCAAAGCAOAGGCTGTACATACCTTAGGCTGACCAT TCCTTTGGGGGGCTGCAAACTGCTTTGAGGAAATNCCAGAGGGAATAAAGTAGAAGACGC ACCTGCTATTTCCACACTACTATGAGAAATACAGCTAATGAAGTGTGGCGAAGCTTGGCCCGTGTGA GTGCCCGAGGGTAAAGTCTCTCTCTGTCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---				AGCCATACAAATGCAATGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT ACATTCATGTCAGGATAAGGAGCAT/GJACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAATATAAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCTCCAGAGGGCTGAGGAGCAGGCGGTGGTGGGAA
WI-20270a	53 G A ---				AGCCATACAAATGCAATGCAAAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT AATACATTCATGTCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCTCCAGAGGGCTGAGGAGCAGGCGGTGGTGGGAA
WI-20622	130 T C ---				CCACTTTCATATTTACAAATGCTCACGAGCAAAATATGAAGCTTCAACACTTTCCCTTTGTA ACTTGTGCTCAATAAATGCACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/GJ TACTAATTTTATGATGTTACTCATATTTTATTCATATACTTTTAAATGACATCATTTGCCAATACATA CATTAATTTCTNTAACTTTATTTTACAAATAGCCAAACATCTGTCAAGCAG
WI-20768b	190 C T ---				TTCCCACTCAAACTCCACCCCAACCTTCTCGAAGCAGGCTAACAGGACCTCTGCGCTGCGTGC TCAGGACTGATTAATTTCAATCCAGCTGCAATGCAAACTGAAACTCAATCTGTATATACCACTCTA CAGGAGAGGTCTATTTCTGGGCGACCCAGAAAGTACAGCAGCATACTGCTGGGAAGCTGAGGACTC GTAATGCGCTTGTCCCACTCTCTATGGGGTTTACTGCGCTCATTC
WI-20768a	71 C T ---				TTCCCACTCAAACTCCACCCCAACCTTCTCGAAGCAGGCTAACAGGACCTCTGCGCTGCGTGC TCACTGACTGATTAATTTCAATCCAGCTGCAATGCAAACTGAAACTCAATCTGTATATACCACTCTA CTACAGGAGAGGTCTATTTCTGGGCGACCCAGAAAGTACAGCAGCATACTGCTGGGAAGCTGAGGACTC GTAATGCGCTTGTCCCACTCTCTATGGGGTTTACTGCGCTCATTC
WI-21909	153 A T ---				TGTTGGCTTTGTCAGGACTACTGCTGTACATAAATATCTCAATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCAGCTAAATAGGAATTTGTTGTCATCTTTAAAGAA TGCTTTAACAATACCAAGATGATGGAATCAATAGAAATATAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAAATAGGATACCACTAAATTTATTTCTATGTATGGAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTGCTTTCTGGAAACATAATGGAAACATTGTTTTCATAGCTGTCTGACAGT GGCAATCCCATCCATCTTCAGGCTTTTAAAGGTCAATATGAATCTGAATTTCTTAAAT ACTCTGGTGCAATTCATTTCTGCAAAAGCAACTGGCAACACCTCTTCCGGTGGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACCTTCACAGCTCAC
WI-22189	70 C T ---	---	---	CCAGGATGAATTTCCACATTTATTTTNCCTTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AACTGAGCGGAGGAATGGGATGCGCTGCGGTACAGCTGGACGTTGTCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGATCATAGAAAAAACCCTCAGCCAGAGTTAGGACATTTGATCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCTCTGCGCTCTGCTGTTGTTGTTTCAATTTGCAAAATAAACCCA GACCGGGTCACTTTCAAGTTCCCTTCCAGCTCTATTTATGTTGCTCTAGTCTTTATGAGCCA TGATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTCTCTGAGGCTCTGCCAGGTGGATTAGTGAAGAGAGTTTATGGCCCTCTAAGCAACCG GCCAGTGTGGGAATGCCACATGCAATGGTGGTGGGATCTGGGGGGGTGAGACCTTGTCTTT TCCTTCCAACTCTCTCTTACCCAGAACTTTGCGAGAGCCCTTTTNAATTTCTCTTCCCTCTATTC CTCTCTTCCCAATGTGCTAAGGTCCAAATCCAGACCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGGAAAGGTTACAGCCATAGTGAGTTCCCCCATTTGCTCAGTACCAGAGTGTGTTGAGTAC GGTCGTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGTCGCTCTCTGCTGGCAGCATCTATACCCACTCTGGCTCTGAAG GCTTGTCAACCAAAATGGGAGCTGGGCTTAAGCATATTTAAACAAGGCTCCAAAGGACCCCTT TCACTGGGTCTAGCATCCAGCCTCTCTCTCAGCAAGGCGAGATTGTGGTCTTCTTGTGTTTCTG AACAGGCCAGGCGGCGAGGCGCATGCCATCCTGCACTGCACTCAACCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTGTGTTTAAATTTCTATACAGAAATGGTTCTTCTTGAATATTT GTAGGATGGATGAATTGAAGTGAATTAAGTCAAGATAAAGGGGCAACTCTTTAAATGAAG GAAATGTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCTTCCAGCTACACTTTACCTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAGTCTGACGATCAGGTCTCTCCACCAAAAGCAAAACAACTGCTGA AATGTGGCAAGTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTGCTTTATGTTTACAGCAATCAAGNTCCCTTCCAGGCAAGCCAGTGTCT CTGGATGGCATCAGCAGAGCTCCCTCCCGGCTTGAAGCATGGCTGTGTGACCAT ATTTCCCTTCTGTGTTCTGTTATTCCTTTTGTGAGTAAATAGCAATACAGTGTCTGGA ATCTGCATGATTAAATAACATTAAAGTTTCAACACACCCCATATCAGCAATGAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATGACATCTCTCCTAGTT T
WI-21342d	59 T C ---	---	---	

UTR- 04932-2a	149 C T	---	---	GCAGCATTCTCTCCAAACCTCCAGGCGAAGCTGGGGCAGAGCACTCATGCGCAGCAGCAC CTACGTGGCCGAGTACGAGCCCGCTGGCCCAAGTTCTGGCTCTCAGGACGTCCACAGATGGA GCCAGAGTTTGTCTGTGGACTCCAGCCAGGGGATGAGGCCGCCGCCAGCAAGCTGGAGTCTC TTTGAGCGGGCGCGCTGCTCAGCTCTCTCTGGAGGTGAGGAAGAGGT
siFIBb	412 G C	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siFIBa	341 T C	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siGLV2	61 T C	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1001 7c	70 T C	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1001 7a	33 G A	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1002 3	63 A T	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1009 6	36 G C	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1011 8	107 C A	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1012 0	89 T C	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG1017 8	42 C T	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCACTCCACACTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGCGCCCTGGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACAGCCTGAGTCTCCATGTGTGTAGTACATCTCCAGATGCGAGCCCGAGGCGCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT

siSG1033	116 T C ---	---	TTTAAAGCTACATGCTCTGAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAGGATGCATTTCGG
1b			GTCCAAACCTGCTCTAGGAAGCGCTAGACCTCAAAACACAACACATCCATCCTGCTCTTTGG
			CTACTATGCTTTTCCGTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCACCTGTTCACTGA
siSG1033	107 A T ---	---	CTTAGGACCTCC
1a			TTTAAAGCTACATGCTCTGAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAGGATGCATTTCGG
			GCTCCAAACCTGCTCTAGGAAGCGCTAGACCTCAAAACACAATCCACCTCCATGCTGCTCTTTGG
			CTACTATGCTTTTCCGTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCACCTGTTCACTGA
siSG1243	225 GA ---	---	CTTAGGACCTCC
b			ATTGGCAATGGGAAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAAATCCTCCTCTTG
siSG1345	60 G A ---	---	AAATATGTTTCAGGCCAGCAGTGTAGCTTATGCTGCAATCCACGACCTGCTGGGAGGCCAAGGAGA
b			AGGATCGCTTGAGCCAGGAGTTCAGACACCGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT
siSG1345	54 T G ---	---	TTTAAAAAAGAAATCTGTTCG/AJAAAGTATTTTCAGACCAAAAAGGAGGT
a			AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTGCTTCTTAC/GA/CGCT
			TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
			AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTGCTTCTTAC/GGCT
			TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
siSG1385	117 T G ---	---	TTAATGTATCAGGAGGGGCCAGGGATGAGGGGAGGGGTGAGGAGCGAGGCGAGTTATTTT
b			TGGGTGGGATTCACCACTTTTCCCATGAAGGGGAGACTGGTATTTGTG/GTCAATCATTAAGAA
			GACAAAGGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGGCTCTAAAAACATGGCC
			CCAGCAGCTTCAGTCCCTCTCTGCTGG
siSG139	69 T C ---	---	TCGTCCTCTTTCAGTGTCTTCTGCCAAGCATCCCATGATGTTGTGACCGCACAGCATTTGTGCT
			TTGTGCTTTGAGCACTTGCACCTTCTGCTGGTGTGCTGCCACTGATGTGTACTGTCTGCTGGCC
			GATCTGTGTCCAGACAGGCTGATTCAGACACTCCACGTGTGAAGGCTCTGTTGTTGTCAATCCT
			TGGCTCCTCCACTTCAGTTTGGCTTTCTGCTCCAT/CJAGTCTCTCTCCATGTGCAAAACAAGATGGC
			TACTGTGTGTCCAGAGTTCACTGCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCTCACTCCCA
siSG1427	103 T C ---	---	AAGTCCATACTCAATCCTTTGGGAAG
			CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTTAGGTCG/JGCTCCCTTGCATGA
			AATGTGGGAGAGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGACCCCTTCCCTATCCTACC
siSG1471	50 A G ---	---	GCA
			CAAAACCAAAATCCTCCACGATATAATTACTATTAGTCTAAGT/GJTAAATTCAAAGGTTGAGA
siSG1483	44 T C ---	---	ATGACGAATTCAGAATTTCTTTCATACATAAATGCTTTCTTAGTTCTGCAGATGGGTA
			CACACCCACAAAGTTTCATGTATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACAGGTGTGCA
			/CJGJAATGTGGAGGATGTCTGTTGCAGCTGTAGTTACTAATGACGGGAAAACCCCAATGCAAGAGGAA
siSG1696	67 C G ---	---	AATGCTGA

siSG1847 b	95 GA ...	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAAAATGAAAGAATTT AGAGGTTAAATAAACAAGTGAGAGACG/AIITTTACTTTACATCAGTTGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTGTGTTCCAAATGTGAAACCAAAATTAATAAATTAACCTGATCAGTGTGCT TCAACACAACTG
siSG1847 a	49 CA ...	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCTC/AICTAAAAATGAAAGA ATTTAGAGGTTAAATAAACAAGTGAGAGACGCTTTTACTTTACATCAGTTGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTGTGTTCCAAATGTGAAACCAAAATTAATAAATTAACCTGATCAGTGTGCT TTCAACACAACCTG
siSG1897 a	83 AG ...	---	CTTAATGCCCTTCTCTCTCTCTCTGACAGGAGACACAGATGGGTAACATAGAGGCGATGGGAAGTGG AGGAGGACACAGGACTTNG/SCCCACCCACTTCTCTCCCGGTCTCCCAAGATGACT
siSG2022 a	86 TC ...	---	TGCTTTGAGGTTCAATCTGAGATATCTATGGCAAGTTTATAAAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATAGATCTGATTCATAATCTCATCTATTAAACATTAACACAGGCCCTTTGTTGT TGTTATTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
siSG2076	104 CG ...	---	AAACGTTGTCCCAAAATTTGTTGAGTTTCAAAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTTATAAACACTTAAGAAATATATTTGACATT/C/GJACATCACAGTGGGCAATTT
siSG2108 c	71 AG ...	---	TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAATGATTC/JGAGGGGCTCCACAG GAGC/JGTTAAGGGGAAGACTTTTATAGGACAACCTGTAGAAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTTCTTATTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTGTTGGGCTGTGCTGA
siSG2108 a	49 TC ...	---	TTGAGCAACAATGATTCGCGAATTTGGCAGCTCCAAACCAAAATGATTC/JGAGGGGCTCCACAG AGAGGACATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTTCTTATTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTGTTGGGCTGTGCTGA
siSG2141 b	173 AG ...	---	TTATCCAGGGGACAAGCTGCACAAAAGGAATGTTCTTATTTTAAACAAATGACTGGGTGTA TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCTGSCATGGCGATGGTCAGGTGGGT GCAGTTCCCTGTGGTCTCTATTGTTGTAAGAGAGAGAAAG/JAAGATTCCTTATTAATATTTAAGGC AGTTTTGAGAGCACTGGCATCTGTTGCTCTG
siSG2141 a	113 CT ...	---	TTATCCAGGGGACAAGCTGCACAAAAGGAATGTTCTTATTTTAAACAAATGACTGGGTGTA TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACCTGG/CJATGGCGATGGTCAGGTG GGTGAGTTCCCTGTGGTCTCTATTGTTGTAAGAGAGAGAAAGAGTTCCTATTATTATTAAAGGC AGTTTTGAGAGCACTGGCATCTGTTGCTCTG

siSG2577	a	121	C T	...	AAITGCCAAATGGAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATCCCGATTGGT CCCAATATAGGCCCTTCGCAAGAAAGAGATCAATCGCGAACCGGAACGATGTAAGAG(C/T)ATGAACAAT CAGGCCAGATTAAATAT
siSG2700		58	G A	...	ATCTCTCGACTGCTTAGTGGGAAAGGAATCAATTATTATGAAGTGTCCGGCCCG(C/G)AAGTCAC TCAGGTTTGGGGAAATAAACCAGCTGGTCCAGAGCAGAGGAGGCTACTTTGAGCCGGACACCA
siSG2724	b	101	T G	...	AAACAAGCTTTTGCAATTTCCACTACATTTGTGTGCTTTTATTATTAATATTGTGCAATGCTATAAT TTAATACATTATTCGAATTCCTTGCAATAACAT(G/T)TTTTTAAATCCTGGGTGTGTGAAGAAC
siSG2776	a	65	G A	...	GTGGCCGATCTTACTTTTCCAGAAAAGGGTAAATAAAACCTGTAGAAAGTCTGAAATATG(C/G) AATATGGCCCTTTTGGATTAGGCCCGCAGAACTTCAACAAGCGACACTGCTGGCCAAACCCACAAA ATATCCAAATTTCCCGAATATAGTAACCCCTGCTTGTCCGAATG
siSG2791	b	109	G T	---	AAGGAAGGTGGAGGGAAGAGGGAAGAATACAAATGGTTAGAAAAGAGCAACTAAAGATTATTTTC TATTACTTCTGAACGGTAAACTAGCAATTTTAAATAATTT(G/T)GGTCCACTTAAATCTATTATA AAGCAGAAAGGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTACAAAAACCAATCAG
siSG2791	a	100	A G	---	AAGGAAGGTGGAGGGAAGAGGGAAGAATACAAATGGTTAGAAAAGAGCAACTAAAGATTATTTTC TATTACTTCTGAACGGTAAACTAGCAATTTTAA(G/T)AAATATTGGGTCCACTTAAATCTATTATA AAGCAGAAAGGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTACAAAAACCAATCAG
siSG2826		85	C T	---	CCGCAATTTTCAACACACATCTATGAAAACTAAGGGTGGATCATGTACAACACAAAAACAAGC TCCCTCCCTCCAAAACAA(C/T)GAACAAAAATAAGAAAGAAAAACCCATGAATGCCCGGTTTAA ATTTTTTTCC
siSG2850		88	G A	---	ATGGGTGCATGTAAAGGCAAAATTAATACTTTTTCAGCGAGGGGTGGCAAAATTTAATGAGCTGA TGTGTCCAAAGGGGAGAGGCC(C/G)AGGCTCACACATCCCATCAATACTCTCCCAT
siSG3031		71	T C	---	ATACACGGGGGGGTGAAGGCATGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT AAAT(C/G)CCCCCTTTATTTAAATGATTCAGACATCTGGGCGAGCATAGCT
siSG3058		81	G A	---	GTCCCACTCTCTCTCTTAGAGAAAAAACTGTGATTACCTCAACTGAATATGAACACTGTGATTG AAAAAGTCAAA(C/G)ATGAAGAAGCATCAAGGCCAAAAAGGCAAACTGGCTGAGGC
siSG3092		94	T G	---	CAGCATCTCCAGAACATCTCTAGAACTGAACCATTCCTGTCACTATTGAAAAACAAGGCCAAGTTC CAAAATCCAAATAATAAATGAACGTG(C/T)GATGATAACAATTCCTTATGGTTCCAGCCCCCTACTTT AGTT
siSG3230		95	A G	---	AAGAAGTACTTTGGTAGCTATTAAATAAGAGGGGGTGGGAATGAATGTGAGATACAGACACCTG CATCTTTAGTCAATTTGTCAGTGGAGTGA(G/G)GTGGGGTGCCTAAGTGTTCGAAGTGAAGTAG
siSG3245		160	G C	---	ACATCTCATCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGAGCCCTGCTCCAGGGGCC CAGGTATGTGTAGAGGCCAAGTGGGGGTGGCCACTTGGTGTCTTCTACCAACCCCTGCGCATCCAGTCTG GCCCGAGTACCTACCTGGGAGGT(G/C)GTGACTTGGCTTAAGTACTTCATGCTTAT

siSG3265	42 T C ---			AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAATGCGCAATGTGTAATGTTCTCAG TTTTCATTATGGAAGATGATGATTTTCAGCCACATTCAGTGTATGTTCTTAAATAACACAATCGAC AGGACTGTCTGTTCAGTACAAATGAGGACAGCTTTTCAGGGCAATGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAA
siSG3269	141 C T ---			TGTACTTACTGTGTGTCATCCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCTATGCTAAA GCATGAICTTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAACT
siSG3269	24 A G ---			TGTACTTACTGTGTGTCATCCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCTATGCT AAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAACT
siSG3284	130 C T ---			TTAACTCAAGAACTTTTCAGTTACAGGAAGTTATCTAATTTAAATGACTAAATTACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCA(C/T) TCCCTAACTTTTGTAAITGCTGTAAATGGGACATTTGTGTTGATCTACCC
siSG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAACTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA/TTTACAAATCAATAGCATTTTCTTAACCTCAA TAAATGTCATATCTTTAGCTCTCACTC/ACCAGTGTATCCATTTTCCCGAGCGGTAGAGCTTTTCTG TTTCTGTAGATTTGCTGCTGCTGGACATTTGATAATAATGGAGTTGCTGTATCATGTGAGCTTCTC ACCTAGCATGATGTTTTCAGACACATCCATGCTGTAGCATGCGTCACTTCTTCTTTAA
siSG3323	26 C A ---			GATCCCGAGTATTATTTCTAAATTTGAATTTGTTGTGGAATAAAAAATCTGAGGACCCTCAGAG GG(C/T)ATAAGGGAACCTCTTTGCTTTAGTTCTATAAGGACTTTCT
siSG3369	69 C T ---			CAAGACTGTAGAAGCTAGGCTGTGTAGAGTGAAGGAGGAGTGTGCTGCACTTGCCTCAGGACTCAGG CTCAGCTTCACAAATCCGAGGAAGGAATGACATTTCCAACTGTCACTTGTAGC(G/T)CTGGGT CAAAGTCTAAGAGGACAAATAATAGAGACT
siSG3398	125 G T ---			TCCTTACTGTTAACTGAGTGTGGAGTAAAGGATGCAATCACG/AGTCTACTGTAGCCTGGACCTCC TGGGTTCAAGTATCCTTCCACCTCAGCACTGAGTAGTGCGCTGCAGGACAAAGTCAACCATGCTA CCTAAGTTTGTAGAGACAG
siSG3416	43 A G ---			GTAAGACAAAGTTTTCGTATGTTGACCAGGCTGGTCTTGAACCTCTGGCTTCAAGCGACCGTACCA CCTTGGCTCCCAAGTCTGTATTTACAGGTGTAGCCACTGCCCGCCCGCTTTTAAACTGAAT GTTGAAAAATCATCTGCTTTGCTGGTAACTGAT/ATCAAGTTGCTTAACTTTGTGAAACCCAC TTTCCCTTATCTGTAACAAAATGGACAAACAACTTTTCCCTTCTCTC
siSG3424	173 T A ---			GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTCAAGTGTGATGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGGCCCT/ATGAAATAGCTTACTCTGTTTCTCTATC
siSG3436	88 T A ---			

siSG3483	103 C T	---	---	GATACAGAAGATAGTGGTATGGATGGATAGTGAAGGACAAATAATACAAATATATTTATTG AAATAAACAATAATGCATACACAGCTCAATGGGTGAC[C/T]GGAAACAACCTGGCTGACTATATTA CTGA
siSG3491 b	71 G A	---	---	CAAGTACTCTATTGCTCTAAGTAGTGCAGTCTGGCAAATATTTCTCAGCAACAAGGACGATTG AAGA[G/A]GTGGAAATCTGTGCAAGGAGTACTTTACCTCCAAATAGCTGCAATTTAGCAGTCTGA ACAATCTTTCTAATCTTTTACTGGCACCTGTGGATTTCTATTAACTCATTTACTATTTTCTGTGATG ACAGAAATAAGTTAAC
siSG3523	33 C T	---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTT[C/T]GCAATATGTGTACAAACACACACACACC CCTAATTCCTCAAAATGCTCTGGCATAAGTTTATCTTACTGGTCTC
siSG3536	213 A G	---	---	AGTACAAACACAGATTTAAAGAGCTCAGAGATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAATGGCTTC TGTGATAGTGGCTTGGTGAACGCATCTCAGTCTCATTTCTATTGTTTATAATTTGTTAAATGAGCTTG TGCACCATTAG[G/T]CTCTGGGTGTTCTCAGTCTTGGCATGAAGTATG
siSG3583	112 G A	---	---	GAAAAGCTTAACATACGATCCATGTGCAAAACCCCAACAGGATCTACGAACCTCTGGCATGATCCA CATGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACTAC
siSG3586 a	60 G C	---	---	CCTAGTAACATAGTGAGACCTGCTCTACTAAAAATTTAAAAATCAGGTGGTGGTG[G/C]ACG CCTGTAGTCCCTACTTTGGAGGCTGAAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
siSG3589	101 T C	---	---	ATATAGTCTGGTAGCATATAAATCCTTTAAAAAGCAATCTGGCCATATCAAGSCAAAAAAGT GTATATACCACCTGGCACAAAAACCCCAATGAT[C/C]CTATTTTCCAAAGATGTATCCAGATGAAA GTATCCAAACAACAAAAGCTATATACAC
siSG3590 a	70 A T	---	---	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGAAGAAATGATCTTCTGTTCTAAAAA AA[A/T]TTTCTGATGCTCTTGACCCCTGAGGAAACACATTCAGTTTCTACACT
siSG3619	78 A C	---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGGAGCTTAAATTTCTTGAATTCATACGCT TCTGTCATT[C/A]ACAACTCCAGAGAAAACTGGGCTCTATATTTAAG
siSG3644	40 T C	---	---	ACATATGAATGAGCTTATAGTGGCATATTTAGGATGAGAT[C/G]GATTGAGAGGATGAACCAAGG ATGCGTAATTAATCAATTATGAATAAAGTTATCTGGGGAACGGCCATTTGTCCAAACATTTACTAA GTGCTACTA
siSG3646 c	70 G A	---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAATATATGATGAACAATAATATGCTTACT GGT[G/A]ATATTAAGCTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGAGATCAIT CTCTCTTTGTA

siSG3646 b	55	A G	---	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATAJAGJTATGTCTT ACTGGTGATATTAACTTTGATACCTTTGGTTAAGATGGTGTCTGCTAATTTTCCATTTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43	A T	---	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATAJAGJTATGTCTT ACTGGTGATATTAACTTTGATACCTTTGGTTAAGATGGTGTCTGCTAATTTTCCATTTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85	A C	---	ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAAACCTGGACTACCT GAAATATCCTACGAGGCACTCGCCCTCCGAGACTGACGATTATTAACCCACACACGGAAGG
siSG3693 a	30	C T	---	ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAAACCTGGACTCA CCTGAAATATCCTACGAGGCACTCGCCCTCCGAGACTGACGATTATTAACCCACACACGGAAGG
siSG3698 b	145	G A	---	TCTTGCCCTTTTGTGTTACCCCTAGAGAGATGGCAACCAATCCCGAGGTTGCTCTCTGACTTCCACAT TCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG(G/A)GAATACCCACCCACCTTCCCTCACTGCAGA
siSG3698 a	51	C G	---	TCTTGCCCTTTTGTGTTACCCCTAGAGAGATGGCAACCAATCCCGAGGTTGCTCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAATACCCACCCACCTTCCCTCACTGCAGA
siSG3724	107	C T	---	ACCAGCCTCATGTGTCAGAGGGTCTCTGCTGATCCCACTGGAGCCATCCCTGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTCTGCTCAGTGTGAAG(C/T)ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTCT
siSG3725	104	G A	---	GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGAGTTAATAGCAGAGTCAACAGCATTTAA ATCAATAATATTATACAGCCCAACAGCAACAGCC(C/G)AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
siSG3751	128	G A	---	CGGAAGAAAGAAACAAATCCACAGGAACAATCTATGTTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAAGTATTTAAAGGGGGAAGCAGGCTGGAGGGGAAAGAGAGAGATATGGTCC(C/G)ATT GCTGACTCCTATGTTGCAAGAG
siSG3787	49	T A	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTTATTAJAAAGTTCCCTAAGA CACTGAGGGCAATAAAACCAAAATAAATAAAGAGTGTAGGCTAAAGAGATATCTTCCCT
siSG3880 b	115	G C	---	GACAGAGAAAGAGATGGCCAGAGACAGGGCTGGGGCAGCTGGGGTCCCTGAGTGGCAGGGGC CACCACACCTCTGTGGTCAAGGCCCTCTCTGGGAGCAGGCTAG(C/G)GCGACGGAGGATGCGAG GGCTGGAGGGGACCCCACTCTGGGGACCCCAAGGAGTCCATTCTGCOCT

siSG3880 a	36	G C	---			GACAAGAGGAAGAGATGGCCAGAGACAGGGCTG/CJSGCAGCTGGGGTCCCTGAGTGCACGG CGCCACCAACAGTCTCTGTGGTCAAGGCCCCCTCTCTGGGAGCAGGCTTAGGGCAGGGAGATGCAG GGCTGGGAGGGACCCCACTGGGGACCCAAAGSAGTCCATTCTGCCCT
siSG3895	44	A G	---		---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTGTA/GJTITTTTTTCCATTAACTAA TACATGCCCTCATAGATATATCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
siSG3902	104	T C	---		---	TCTGTGAGACTGGAGAGACAGGTACCAAGCAGGCTCTGGTGGGAACCTGGCTTCTCTGATAACA TCATCTATTTCACCTAAATGTGAAGCTGCTTCTTTTC/JCJGAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTCCTGGACAAT
siSG3935	50	G A	---		---	GGGTGTCTGACGGAGGACACCCAGCAGTTTCAACAAGCAATTTGTCQ/GJCTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGTCAACAACCTTCTCGAGCT
siSG40	25	A G	---		---	GAGGAAGAGGTTGAAGAAGTGTGA/GJAAATATATTTAAGATTTCTTGGGGAGAAATCTCGTGC CCAAACCTGTGTGATGGATCCCTTACTATTAGATAAGGAACAATAAACCTTGTGTATGTATCA CCCCAA
siSG4009	32	A G	---		---	GTGTGGCTGTCTGATGATGAATGGCGCTCJAGJTAGCTTTTACGGTCTTACACTTTTATGTCCT ATGAATTCCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTTCCACACTGCTTACA
siSG4033	123	T C	---		---	AGAAGCCTTGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAGCTACAGTGCAGTAACCAAGAACCTTAATGTTTTCAAGCATAAAGGTACTTTT/CJGTGAAC AGTGGGCAACAC
siSG4038 a	29	G A	---		---	GCTGAGACAGTGTACAGCCAGCCTGTG/JCJGAGGCCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCACTGAGGTTCCATCACT
siSG406	53	T C	---		---	ACTGTGTTCAACAGTATTGCGTTGTGAGAGGAAAGCTAAACGAACAAAT/CJGGTTTTAGTT TTGCTGAAGACTGGCTTATTAATGGACAGCTTTCTTAAACAAGAGATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55	G T	---		---	ATCTGGCTGAATTAGTCAAGCAGGTCAAGTACTATTGTCTGATGATGATTAG/GJTAAAAAA GTTTGCTGTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCAITGGCCCTTCATCCTGG
siSG4095 a	27	A C	---		---	ATCTGGCTGTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCAITGGCCCTTCATCCTGG
siSG4120	65	G A	---		---	TGCATGTTCCACATCTTTCATAACGCAAAATGTATAATAAACTTACGTACTTATGGATAATAC/G/ ACTTTTCCCTCAGAGAGCCACAGTTAAACAGTTCCAGCACACCATTAATCCACCGAGCT

sISG4128	54	A G	---		CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCTJW/GTATATTT TACTTCTTCTGAAATGCCCACATAATTTTGAATAATGATTCACTCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCCAAATGTTCCAGAGGG
sISG4209	128	G A	---		CACGAAACAGATGAGCCTACACAGTGCTGTAGGACCGAGGCTCACAAACATCCACATGCGCACAAAGC AGGGCCGCGCCACTCCAGGCAACAGCAAGCCACCCCGAACCCTTGCAAGGCGCGCAGCTCCCTCTG/AGC AGGGGACCAACGAGCGGACAGAGTGCTTTGATGCTDCGAAAGAGCTGAGCTCCATTCCA
sISG4209	65	G A	---		CACGAAACAGATGAGCCTACACAGTGCTGTAGGACCGAGGCTCACAAACATCCACATGCGCACAAAG /ACAGGGCGCGCCACTCCAGGCAACAGCAAGCCACCCCGAACCCTTGCAAGGCGCGCAGCTCCCTCTG/AGC AGGGGACCAACGAGCGGACAGAGTGCTTTGATGCTDCGAAAGAGCTGAGCTCCATTCCA
sISG4254	31	G A	---		CAITACCCAGAACGCGCATGAGGAGCAGAGCG/AGCAGGCGCGGAGCTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGCGCGGGGCTGCTCCCGGAGGCGGCGAGCGTGAC TGGGGGACCATGGCGGAGAGAGGATGACCGGGTCATG
sISG4301	81	T G	---		TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACATTTCCAT TTAAGCAAAATAAATJTG/AGCTTCTGAGTAGTTGTCCCGAGTTTCAACCAACATTTG
sISG4331	71	T G	---		CTCACAAAGGCCAACACAGAAAGATACAAATACATTTCACAGCTAATATTTAGTTTATGACAC AGAGTGTGTTTCAACAAGTTTAAAGTGTCACCTGAAGAGCATGTTAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTGGCCTCGCCCTGTGTGATCTGTTTGAGGGGTGTGC
sISG4340	76	G A	---		TTTTGCAACAAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTATGATACAGAAAGTCAAAACC ACATGTTCTG/ATTAAGTGGGAGATAAACAATGTGTACACCTGGAGCTGGAGAGCAGAA
sISG4361	109	A C	---		TTCCCAACCATGAGTGACAGAGCT/PCAGTCAATGCAAGTCAAGTTCAGTCAAAATTAGG CACAAGTCTTGGAAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTGAGG
sISG4361	24	T C	---		TTTCACTGCTACTGTGGTGCTGTGCTGCTCAAACTGCTTTTSCAAGTGCTTCTCCAAAGGGGAG AACAGTGTGGAAGTGGGCTGTGCAAGAGGCCATTCTTCCAAAGGCCATTCTTCTCAGCTGC
sISG4376	73	A G	---		GAAGGCCACAACACTCCTAGCCAGAGATGACAAACATACGATTTTCTT/CTCAGTCTGTAGT ATCCACAGTAGTGTCTGTGTCATGTACAAAGTGTCTGCCAGAACCCCATTAATTCATGCGC
sISG4381	50	T C	---		ACCAATGGTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATAGTGCAGGGCTTAACCAT TCAACACCGG/AGJTGACACGAAACCCAGTGGACTGTGAAACTCAGGCTGCAGGGGTGGCTTGT CAGCTGGGT
sISG4410	79	A G	---		

ESTD-AT3a	..	--	---	---	---	AGACCTCAGTTTCTCTCTGTAAAAGGGAAGTTTGTTCTTGGATCTCCATGGGCCAGCCAGCACTGTGTCCTGTGAGTCTGTATCAGAGTATGAGGAGATGGGACAGGTGAGAGGAAATTTGAAAGGCCATTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAAATGTGG
ESTD-B3aR	..	--	---	---	---	GGCTGCCAGGGGTTCCGTGGGAGCGGCCCTAGCCCGGGGGCCCTGCTGGCGCTGGCGGTGCTGGCCACCGTGCGAGGCAACCTGCTGTGATCCGCCGACTGCCGAGACTCCAGACCATGACCAACGTTGTCGTGACTTCGCTGGCCCGACGACCTGGTGATGGGACTCCTGGTGGTCCGCCCGGGCGGCCACCTTTGGCGC
ESTD-B4S11	..	--	---	---	---	GGGCAACATAGTGAACCCCATCTCTACAAAAATACAAAAATAGCCAGGTGGTGTAGCAAGTGCCTGTAGTCCCACTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAGTGAGCCAAAGTGTGCCACTGCA
ESTD-BCL2	..	--	---	---	---	AGCTGGATTATACTCCTCTCTCTCTGGGGCGGTGGGGTGGGAGCTGGGCGAGAGGTTGCCGTTGGCCCGTTGCTCTCTCTGGGAAGGATGGCCACGCTGGGAGACAGGTACGACAAACCGGAGATAGTGTGAAGTACATCATTAATAGCTGTGCGAGAGGGGCTACGAGTGGGATGGGGGAGATGTGGGGCGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCATCTTCTCTCCCA
ESTD-BCR	..	--	---	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCATAGAGCCCGGAGACTCATCTCTGCGCAAGAAGCAAAAGAGTCACTCTGTGTGTCGGGGGAAGGGAGGAGGAGTGACAAAGCTAACTGCTCTCAAAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA
ESTD-BRCA1a	..	--	---	---	---	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAAATGCTGAAGACGCCAAAGATCTCATGTTAAAGTGGGAAGGGGTTTGCAAACTGAAAGATCTGTGAGAGTAGCAGATTTCACTGGTACTGTGTACTGTATATGGCACTCAGGAAGATCTCGTTACTGGAAGTTAGCACCTTAGGGAAGGCCAAAAACAGAACCAATAAT
ESTD-BRCA1b	..	--	---	---	---	ACTAAATGTAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCATGTCACTGAAGAGAAATGGAAATGAGAACATTCCAAGTACAGTACAGTACAGCAAAATTAGCCGTAATAACATTAGAGAAAAATGTTTAAAGAGGCCAGCTCAAGCAATTAATAAGTAGAGTTCCAGTACTAATGAAGTGGGCTCCAGTA
ESTD-BRCA1c	..	--	---	---	---	TTAATGAAATGCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATACCTAGTTTCTGAAATGACATTAAAGGAAGTTCTGCTGTTTTTATGCAAAAGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCAAGAATAAGAGTCTCAGAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	..	--	---	---	---	ACACAGGTGCTGGCACTGGGGCTGGGATCCTCTCCCTAATTTGCTCCGGGAAGCACATTCATCAACAGTCAAGTGGGGACAGCCATGCACTGAGCCCTGTGGTAGCCCTTTCACCAAGTGCATTCCTCATCA
ESTD-C2	..	--	---	---	---	GCCTCTGCAAAAT

ESTD-C7	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	GGCAAGTTTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACCTGGAAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAAATGGGGAGTGCACCAATAGGGGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGCTTCTTATGTTGCTTTTCCCGGCTTCTCTCACACAC
ESTD-CB23	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGTTCTTTCCGGGCTTCTCTCACACATACAGAGGCCCCCTACAGGACGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTTTCCACCCGA GGTGGCTGTTTGGGCCATCAGAGCAGAGATCTCCACACACCAAAA
ESTD-CB24	ACCAGGACCAAGAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCAGGCTGCTGTGTTTGGCCATCAGAGGAGAGATCTCCACACCCAAAAG GCCACACTGATGCTGGCCACAGCTTCTACCCGACCCAGCTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTCAGCAGACAGCCGAGCCCTCAAGGAG
ESTD-CB25	GTTCCTTTCAGAGTGTGGCTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTATCTTTCGCGCTC TCTGCTCTGAAACCAGGGCATGGGAATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTTGTCAACAGAGTCTTACCAAGCAAGGGTCTCTCTGCAAC ATCCTCTATGAGATCTTCTAGGGAAGGCCACCTGTATGCGGTG
ESTD-CB27	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGCCCTGGTTGCATTTCAGGAGTGTCTGGAGTCTGCTGCTCACTGACCTATCTCTGA TTTAGGAAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCTGCT TTCCTCTTCATCCTGATGGAAGTCTCTCAACACCCATTTCCTATACC
ESTD-COL2A1c	AGAAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTGCTGCTCTTCAAGGGTGTCAAGGTGGAAAGGT GAACAGGTCCTGCTGCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACATGCTGCTTGTG GTGAGCTATTGAGCTGTAATCACCATACCTGACCT
ESTD-COL2A1d	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGAACCTATCTAGGGC AATAGACTGAGTTTCTGGGACCTGGAACTGGACTTCTTCTACTGACGACAGCAAGACTTACCC AAGAGAGATTAAAGGCAAGATACAAATACAAATTTTATTTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	GGCGCAATGCCGGGAGTTTCTCAATGTGTGGAGAGGCTTGAAGACATGTTTGAATGCTTAGAA GGCAAAATCCATCAAAAGTTAACTTCTGGGCAAGATGAAGAGCTACCATCTCTCTCATATGAAGAC TGGGAGGCGCGCATAGTCTCATGCTGTAATCCAGCATTTTGAAGGCTGAGGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAACCAACCTGGCCAAACAT

ESTD- CTLA-4	--	--	---	---	---	ATGGCTTGCTGGATTTCAGGGGACAAAGGCTGAGCTGACCTGGCTACCAAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTCTCATCCCTGCTCTGCAAAAGCAATGCACGTGGCCCAAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAAAGCCAC
ESTD- CYP206	--	--	---	---	---	CAGCCAGCGTGGTGGAGGTGCACCATCCCGGCGAGAGAACAGGTACGCCACCACATATGCACAGGT TCTCATCATGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	---	---	---	AAAAAACATTTTAAACACCTTTTCAATCATATACACCAATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTTCCAAATTAATCTGCAATCTAAATGTCTAAATGATTAATGCAAGTTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGAATTAATTTATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	---	---	---	CATCCCAAGCCCTCCTTAGCCACTGGCATTTTTCGGCCCTTGACAGATACACTCAGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGGGGTG GGTTGTGGCTATGTGGTGGTCTTGTGTAGACGGGGCTTGGTTTCAGTTGCACATTTGCGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	---	---	---	TTTGAGACACCCCTGGCCAAACATGGCGAAATACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCTATCGTAATCCAGCTACATCGGGAGGCTGAGGCGAGGAAATGCTTGAACCCA GGAGCAGAGCTTGCAGTGAGCCAAAGATCACACCTGCATTCAGCCCTGGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	---	---	---	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGGCATCTTAAAAATCCAAATAAGTACACTGTAAATAAGAAATTTAACAGAAATATCATTTGT TTATCAAATATTATACATTTATTTTATTTGTTAGCCATACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	---	---	---	AGGTTCCACATTATGCTGATGTTGCTGATGTTTCCAGGAGCCTTGATGTCATCTGTATCTCCTCAG GTATCCCACTTTGAGACGTACTTTTCAAAAACCTCTCTACAGCGGTTGTGTTATTAAATCAAGGTGA ACATAAAGTA
ESTD- D3S2	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGCCAGCCCTGTAGCAGAACATTTCTCTGC TGAGTCTTATTTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCCC AGAAGTGAACATACTGCTCTAGAGCCAGAGTACACTGGATGTTCTGTTGGTCTTCACGATGG CAGGTATGAATATAATAATCTGCTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	---	---	---	TTTCTGTTTACCTTTGTCAGATCCTTCAGAGGAATCCCTATATATGGCAGTATATGAAATGTATTT CTTAAACAAATAACTTGAAGTCCAAAATTAATCTCTTGATCCATGGACTGCAAGTAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCAATGTTTCATCAGAGCCCTTGGGTGACCCAGGTGATT GCCAATAAGCAGTAATATTGTAGAGGAATCTTTTTCATGACAGTAG
ESTD- D4S95	--	--	---	---	---	CTTTTCATGCACGATAGGCTTCTCTACTAATCAGAAATTTGAGAAAGAGCAAAACAACTTTCAAGG ATAATGGGCAATCACTTCTTCTTTTAGAGTCTACCCGG

ESTD- G00H	..	--	---	---	CGCAGAACGGTCACTGTGGGTCGGAGTGTGAGGGGAAGGAGGAACTGGGGTTTAGGGACT TTCCGGGGTGAATTTCCCGTTCTGTCTTGAGAGAAAGCGGAGAGCAACACAGCAACTGGCTAA GTGTAAGGAGACCTCTGGTCCGACCGGTGTCTGTCTGCTGCCCCCTGTACGCTGTCTGTCTGCGGAGTCGA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	..	--	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCAACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGCGAGGAGAAATCCGCCACCCACACCTGGCTGG AGCAGAAATGCGAGCGGCGCTGAGCCCGAGGAAGCAGGCTAGGATGTGAGAGACACAGTCAAC TGCAGCCTAAATTACTCAAAGCTGTCCCGAGGTCACAG
ESTD- GNAT2	..	--	---	---	GACCCGTAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACACAGGCATCATTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPK2L	..	--	---	---	AGTCTTCATCTGGGTGTCCAGGTAGATCCCTTTACCCGCCGAGAACTGCTCGATATC
ESTD- HRAS	..	--	---	---	CTGGCTC30003CAGCAGCTGTCTGGCACCTGAGCGCGCGGCCAGGCTCACTCTATAGTGGGGTGG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	..	--	---	---	TTGGAAAGTTCTCCACTGTAAACCCAGTCTATGTGGCAATGTGGCCTGGGCCACATCTGGCCCTG AGGGCCCTGCGAGGCCCCCAAGAGGCCGCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACAAAGCTATGATAACCTTAATTACACCCGTAGCAAGAGTTCCGGCCTCCCGCTTGATTCC AGATGGAGCTTCTTTATCCCTGATGTATGGATTGGCTTCCCTGCTG
ESTD-HT2	..	--	---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTATTATTTGACTTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAGAGATGTGTTACAGTTTGTACAGATTTGTACAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGGACAGCA AAGCGCAGTGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	..	--	---	---	ACCAACGAGCGCGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCAATTT CTGATAAAGTGGTCTTGGGTGCCTCTATCGGCAAGATGCGTACTTATTTGAATAGTAGGTA ACCACAGCCCAAGAGCTACTGAGACTGGCAGCTCTGCGAGCGCGTGAACCCCGTAGCCTAAA TGACAGCCGAGAGCGCGAAGACATGCAATGTGC
ESTD-HT5	..	--	---	---	AACACAAAGCCCGAGCAAGATTAAGCTCGCGACCCCTGGTTTACAGACACAGTCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTGGTTTCTTCTTCTTCTCTTCTATAGATTGATTGCTCTCTA GCATTCGGGTACCGAATAGGATGTAGTTGAGTAAATTCAGGATATCTCTACAAAATGAAA ACATTTTGTGTCTGTAAATCCCTCGAAAAGTTCT
ESTD- GFBP1	..	--	---	---	ACCCAGTGGAGCCCGCTCATTCGACGGTCTTGGCAGGAGTGGCCCTGGGAGGAAGAGAGATGTC CAGGGCACACATAGCTTAGTGAGACTC

ESTD- IGHV4-6	TTTACTATTTCAATGGATACAGAAATTGTTGGGAGTCACATATTCCTATGAACAAAAATTCAGATTT CAGTTTAAGTAATGTTGCTTACATTTGTTGAGTGACGGGCGAGTGGTGATCGGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGTATACGAACGTGAAAGT ATGTAATACTTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	CAAAGTAAGCAACCAATAAATGTTAGCTATTACTATCATTTATTATTATTATTATTATTATTG AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGCACAACTCTGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCTCTGCTCAGCTCAGCTCCTGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTGTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCTGCTGTGTTAGGGTGT GGGTCTCTACCTTGGGTGCTGCTCTGCTCAGGAGCTCTCTGCAATTGCAGG
ESTD- KRT10	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTAAAGTAACCTGCTAAGGTTTTTCCATTAAACCACATATTCTTAAG AGAAGTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATAAAGTTATAACCAATTTGATA
ESTD- KRT8	ACCTCACCCCTCCTTAGCCGTGGGAGGAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGACACCTTTGAGAGTCTTAACAGCAGGGCCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAAGGTCAAGACTAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCATAG GCTGCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF78	GGGTGATTTTGAGGCTCAGTTAATATTCAAAATTTGAACGCTAGCAAAACTGCATGGTATTAGA AAATAAAAAATTTCCAATATGTAGTGTGTATACCTGCTCTGCCATGCAGCATATAGCCTGT GGGAACAGGAGGGCTTCCCTACCACCCAGA
ESTD- LMP2	TACACACTTTCCTTACCCATTCTACTGAAAACGACTCGCAAACTGGAGCCTTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-ILPL	TGTCAGTGTCCCTAGGGGCACTCACCACCTCCAGCTCTGCTCCCTGCTGCTGCTGCTGCTGCA AGGTTTTGCTTAATCTCAATCAATGCTCTTCATCTTTAGCAGCTGTGGGGTTTTGTTGTTGTTG TTCTTTTTGCTTAGTATCTGACTACTTTTTTAATATAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACACATTTATAAAAAATTTTTCACCTG
ESTD-MCC	TTGTCAGGAGTGTGCTGATGCTGCTCCCAAGCTCTGCTCCCTAGCCGAACCTTCAGCACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAGGAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGCTTTCCAAAGGTTTGGTCTAAGTGTGCTGATTAACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGTTCTGTTTGTAGCATGG
ESTD-NF1	ATTATCCAGATGAATTTACAAAACACTATACAGATCCCAAGACTGATATGGCTGGT

[illegible]

EST11458 6	---	---	---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCCTCAGTGTCTCATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTTCAGGACGGACCTGTCCCAAGCCAGATGATTACCATTTTCACAGTGGT CCATTAAACATTTCTATGAGCCAGGAGAGATTAACGTATTCCTGCAAGCCGGCTATGTGCC CGAGAGGGATGAGAAAGTTTATCTGCCCTCTCAGAGGACTGTGGCC
EST39852 8	---	---	---	---	CGGTCTTCTTCCAGGTATTGTGCAAGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTAGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST6248 0	---	---	---	---	ACCTGGTGTGCTGTGGGTGAACCTGGTCTCTTGGCATTTGCGGCCCTCTCTGGGGCCCGTGG TCCTCTGGTGTGGGTAGTCTCTGGAGTCAACGGTGTCTCTAGTGAAGTGTGCTGTGATGGCAACC CTGGGAACGATGTTGCCCGAGTGGGATGGTCAACCCGGACACAGGAGAGCGCGGTTACCCCTGG CAATAT
EST38027 2	---	---	---	---	AGTGACTTCCAAGGAATGGCTACCCAACTTGCCTTCTGCGCTGTGGCCAACTATGCTCTCAGA ACATCACCCTACCACGTCAAGAACAGCATTTGCATACATGATGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCAATCTACAGGGCTCTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTTCACTTACACT GTTCTTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGGAAGACAA
EST12274 0	---	---	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGTCTTCCAAATAGAGCCCTTACCAAAAGTGTAT TACATAAAGATCAAGTGGTTTTACTCTCTCATGACCAATAATCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCCGATGGGGTCAGAACTGTTCTCTGTCACCATGGAGGATACTATAACTGTGGAAGATAA ATTCAAGCCACAGACTTGGCAGATC
EST76807 EST44438 7	---	---	---	---	ATGCTAAGGGGATGAGACATGAAGAACCTGTGAGCCGATTTGCTATCTCCAGCCGCCCTGTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCCAAGGCACCTGGGCTCTGGAGGACTCAOCCACTGCCCCCT GCTGCCATGTGGACTGTGTCACAGTTGAGGACTCTTIG GCAGCCAGGAGCCGCTGCAACCATGCCCCGATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCTT GCTCCGACCTAAGCCGAGCAGCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3	---	---	---	---	TGCAAAACACAAAAATCTCTCCAGATGCCCTATGGGTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGATTTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGGATGATTTACTTGTAGTAAGGAACTTGAATGTTATTCAACTGG ATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATAGCTTAG
EST54419 8	---	---	---	---	CTTCTGCCATTTGAATGATTTGTTGCTGTGGGACCTGAGCACTTTTATGGACAAATGATCACTA TTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGGCTGCTATGTGCTACTA TAGTCCAAAGTGA

EST65258 8						TGCCCATCAGCGGCGGAGACATGGCTTGCACAGCTCTTGAGGATGTCACCAATTAACCGAAAT CCAGTTATTTTCCACCCCTCAAAATGACAGCCATGGCGCGGGTCTTCTGGGGGCTCGTGGGGGG ACAGCTCCACTCTGACTGGCAGACTCTTGCATGGAGACTTGGAGGAGGGGCTTGAGGTGGTGAG GTTAGGTGGTGTCTTCTGCAAGTCAAGACATCAGTCTGATTAA
EST38216 3						ATGCGAGGATGAAGGTGGACAGGAGGAGGCGCAACCTGTCATCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTTGTACCCCACTGACCTCCATGACATCAGGG
						ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTTGTAGCATACCTAA TTTTTTCCTGCTCCATGAGACTGTAGCTTTTACCTTAATCTTATTTTAAATGACAGTGGAAG TTTTTTTCTCGAAGTGCAGATATCCAGAGTTTGTGTTTGTGAATAGCAATGCCTGTGAAAAA GAAACTGAATACCTAAGATTCTGCTGGGGTTTTGGTGATGCA
EST62782 9						GAGATCGGTGTGAGTTATTAGGCATGTTACCTGTGATTCCTCCAACTTGTGGGTTCCACCGATG GAATCGCGCAATCTCTGACACGTGTGACCCAGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACAGCAGCGGGATGGGCGCAGGAAGAGCTGCCCTGGATGAA GGAAGAGATTAAAGAGCTTGATTGGACAATCTGGTCTTGGAGTGGAAAGATTCAATGCTCT GCCTGAGTTACACACAGAACTCTTGTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTAA
EST35879 5						GGAATATTAAAAATATTTTAAATACCTCCATTTTGTCTTATCTCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTGATGTGCAATTTGTTCTTACAAAATCGGATGGAAATCT GTTAAGTAACTACTGTTTGCCTTGAATTTGGATTTTAAATGATGATTTATCAT
EST68308 6						ATCACAGGTCTCTGGTCTCTGGCCATCTTCTTGGAGAGATGGATGGTGGTCTGCAAGCCCTTTGG CAATGTGAGATTGATG
EST52908 0						AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAATGAC
EST19590 7						TGAAGCTTCTGCCAGCTTGCAATTTCTTAGGAGAACCCTGTCATACCTTTATCTATAGCCTTCCCC TAGGCTCT
EST76136 0						CTCTGATGGTTTACAGGTGGCAGGACAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTACTGGAGAACAGGACCCACATGGCGGGGATGGCGGGGAGTTCTGGT TGGCGCACCGCTGTGGCTGTGTGAACGTAGCTTTGCGGTGGATGCGATCCCTAAACCTTTGTTCT TGGCCAAAGGAGGGGGGTGGCTGCTGAGATGTAGATGCGGOC
EST58607 0						Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.